



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 5 : C12N 15/15, 15/58, 15/62 C12N 9/70, C07K 7/10 C12N 5/10, 1/19, 1/21 A61K 37/64, 37/54		A1	(11) International Publication Number: WO 91/09125
			(43) International Publication Date: 27 June 1991 (27.06.91)
(21) International Application Number: PCT/GB90/01911 (22) International Filing Date: 7 December 1990 (07.12.90)		(74) Agents: SHEARD, Andrew, Gregory et al.; Kilburn & Strode, 30 John Street, London WC1N 2DD (GB).	
(30) Priority data: 8927722.2 7 December 1989 (07.12.89) GB		(81) Designated States: AT (European patent), AU, BE (European patent), CA, CH (European patent), DE (European patent), DK (European patent), ES (European patent), FI, FR (European patent), GB (European patent), GR (European patent), HU, IT (European patent), JP, KR, LU (European patent), NL (European patent), NO, SE (European patent), US.	
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(54) Title: PROTEINS AND NUCLEIC ACIDS

(57) Abstract

Relatively inactive fusion proteins are activatable by enzymes of the clotting cascade to have fibrinolytic and/or clot formation inhibition activity. For example, a fusion protein comprising two hirudin or streptokinase molecules, linked by a cleavable linkage sequence, may be cleaved to yield anti-thrombotic hirudin or fibrinolytic streptokinase by thrombin or Factor Xa. Fibrinolytic or clot formation inhibition activity is therefore directed to the site of clot formation.

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1 PROTEINS AND NUCLEIC ACIDS

2

3 This invention relates to proteinaceous compounds which
4 can be cleaved to release fibrinolytic and/or
5 anti-thrombotic activity. It also relates to nucleic
6 acid (DNA and RNA) coding for all or part of such
7 compounds. In preferred embodiments, the invention
8 relates to fusion proteins produced by linking together
9 fibrinolytic and/or anti-thrombotic proteins with a
10 cleavable linker, their preparation, pharmaceutical
11 compositions containing them and their use in the
12 treatment of thrombotic disease.

13

14 The fibrinolytic system is the natural counterpart to
15 the clotting system in the blood. In the process of
16 blood coagulation, a cascade of enzyme activities are
17 involved in generating a fibrin network which forms the
18 framework of a clot, or thrombus. Degradation of the
19 fibrin network (fibrinolysis) is accomplished by the
20 action of the enzyme plasmin. Plasminogen is the
21 inactive precursor of plasmin and conversion of
22 plasminogen to plasmin is accomplished by cleavage of
23 the peptide bond between arginine 561 and valine 562 of
24 plasminogen. Under physiological conditions this
25 cleavage is catalysed by tissue-type plasminogen
26 activator (tPA) or by urokinase-type plasminogen
27 activator (uPA).

28

29 If the balance between the clotting and fibrinolytic
30 systems becomes locally disturbed, intravascular clots
31 may form at inappropriate locations leading to
32 conditions such as coronary thrombosis and myocardial
33 infarction, deep vein thrombosis, stroke, peripheral

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1 arterial occlusion and embolism. In such cases, the
2 administration of fibrinolytic and anti-thrombotic
3 agents has been shown to be a beneficial therapy for
4 the promotion of clot dissolution.

5 *

6 Fibrinolytic therapy has become relatively widespread
7 with the availability of a number of plasminogen
8 activators such as tPA, uPA, streptokinase and the
9 anisoylated plasminogen streptokinase activator
10 complex, APSAC. Each of these agents has been shown to
11 promote clot lysis, but all have deficiencies in their
12 activity profile which makes them less than ideal as
13 therapeutic agents for the treatment of thrombosis
14 (reviewed by Marder and Sherry, New England Journal of
15 Medicine 1989, 318: 1513-1520).

16

17 A major problem shared by all of these agents is that
18 at clinically useful doses, they are not thrombus
19 specific as they activate plasminogen in the general
20 circulation. The principal consequence of this is that
21 proteins such as fibrinogen involved in blood clotting
22 are destroyed and dangerous bleeding can occur. This
23 also occurs with tPA despite the fact that, at
24 physiological concentrations, it binds to fibrin and
25 shows fibrin selective plasminogen activation.

26

27 Another important shortcoming in the performance of
28 existing plasminogen activators is that re-occlusion of
29 the reperfused blood vessel commonly occurs after
30 cessation of administration of the thrombolytic agent.
31 This is thought to be due to the persistence of
32 thrombogenic material at the site of thrombus
33 dissolution.

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1 Anti-thrombotic proteins may be used in the treatment
2 or prophylaxis of thrombosis either alone or as an
3 adjunct to fibrinolytic agents. Suitable anti-
4 thrombotic proteins include hirudin, activated protein
5 C and anti-thrombin III.

6

7 An alternative approach to enhancing fibrinolysis and
8 inhibition of blood clotting has now been devised which
9 is based on the use of fusion proteins cleavable to
10 achieve release of fibrinolytic and/or anti-thrombotic
11 activity at the site of blood clotting. To achieve
12 this, proteins involved in fibrinolysis or inhibition
13 of coagulation are joined by a linker region which is
14 cleavable by an enzyme involved in blood clotting.
15 Examples of proteins which may be incorporated into
16 such a cleavable protein include tPA, uPA,
17 streptokinase, plasminogen, activated protein C,
18 hirudin and anti-thrombin III. Fusion of such proteins
19 to a protein with a favourable property not directly
20 related to dissolution of blood clots, for example
21 albumin which has a long plasma half-life, may also be
22 beneficial. An advantage of this approach is that
23 thrombus selectivity of fibrinolytic or inhibition of
24 clot formation activity is achieved by way of the
25 thrombus-specific localisation of the cleaving enzymes.

26

27 According to a first aspect of the invention, there is
28 provided a fusion protein comprising a first sequence
29 and a second sequence, the fusion protein being
30 cleavable between the first and second sequences by an
31 enzyme involved in blood clotting, wherein after the
32 fusion protein is so cleaved the first and second
33 sequences, or either of them, has greater fibrinolytic

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1 and/or anti-thrombotic activity than the uncleaved
2 fusion protein.

3

4 The fusion protein may be a cleavable dimer of two
5 fibrinolytic and/or anti-thrombotic proteins, such as
6 hirudin or streptokinase. It may be a homodimer or a
7 heterodimer. The fusion protein may have substantially
8 reduced or no fibrinolytic and/or anti-thrombotic
9 activity compared to the cleavage products, but a
10 certain amount of activity in the fusion protein can be
11 tolerated. It is not necessary for both the cleavage
12 products to have fibrinolytic and/or anti-thrombotic
13 activity, but it is preferred for them to do so.

14

15 The fusion protein is not restricted to being a dimer;
16 it may have any number (such as three, four or more)
17 sequences which are cleavable one from the other,
18 compatible with the therapeutic utility of the protein.
19 At least one, and preferably more than one or even all,
20 of the sequences resulting from the cleavage will have
21 greater activity than the fusion protein, or a
22 combination of some or all of the cleavage products
23 will collectively have such greater activity. In any
24 event, cleavage will result in a net increase in or
25 release of activity.

26

27 Proteinaceous compounds in accordance with the first
28 aspect of the invention, are therefore cleaved to
29 release activity in at least one of two ways. First, a
30 compound may be cleaved to release fibrinolytic
31 activity. Secondly, a compound may be cleaved to
32 release anti-thrombotic activity. Conceivably, a
33 compound may be cleaved to release both functions. It

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1 should be noted that a released fragment of the fusion
2 protein may have fibrinolytic activity directly (in
3 that it lyses fibrin) or indirectly (in that it causes
4 activation of a molecule which leads to lysis of
5 fibrin).

6

7 One preferred proteinaceous compound which is cleavable
8 to have enhanced anti-thrombotic activity is a fusion
9 protein of two hirudin molecules linked (for example
10 carboxy terminus to amino terminus) by a linker amino
11 acid sequence cleavable, for example, by Factor Xa.

12

13 Hirudins are naturally occurring polypeptides of 65 or
14 66 amino acids in length that are produced by the leech
15 Hirudo medicinalis. Hirudin is an anticoagulating
16 agent which binds to thrombin and prevents blood
17 coagulation by inhibiting thrombin from catalysing the
18 conversion of fibrinogen to fibrin, thus preventing the
19 formation of the protein framework of blood clots. The
20 binding of hirudin also prevents other prothrombic
21 activities of thrombin including activation of factors
22 V, VII, XIII and platelets. There are three principal
23 variants of hirudin (named HV-1, HV-2 and HV-3).

24

25 Another preferred fusion protein comprises two
26 streptokinase molecules linked (for example carboxy
27 terminus to amino terminus) by a linker amino acid
28 sequence cleavable, for example, by thrombin.

29

30 Streptokinase is a 414 amino acid, 47kDa protein
31 secreted by many pathogenic streptococci of different
32 serogroups. It is a plasminogen activator but, unlike
33 mammalian plasminogen activators, it is not a protease

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1 and it activates plasminogen by forming a binary
2 complex with plasminogen (SK-plasminogen) which
3 functions as an activator of free plasminogen.
4 Streptokinase is effective in inducing clot lysis in
5 the treatment of myocardial infarction and is widely
6 used for this indication.

7

8 Cleavable fusion proteins within the scope of this
9 invention may have reduced fibrinolytic and/or
10 anti-thrombotic activity compared to their component
11 molecules; cleavage releases the component molecules
12 which possess to an adequate degree the activity of
13 their wild-type parent molecules.

14

15 The blood coagulation mechanism comprises a series of
16 enzyme reactions which culminate in the production of
17 insoluble fibrin, which forms the mesh-like protein
18 framework of blood clots. Thrombin is the enzyme
19 responsible for the conversion of soluble fibrinogen to
20 fibrin. Conversion of prothrombin, the inactive
21 precursor of thrombin, to thrombin is catalysed by
22 activated Factor X (Factor Xa). (Thrombin is also
23 known as Factor IIa, and prothrombin as Factor II.)

24

25 Factor Xa is generated from Factor X extrinsically or
26 intrinsically. In the extrinsic route, Factor VII is
27 activated to Factor VIIa, which generates Factor Xa
28 from Factor X. In the intrinsic route, the activation
29 of Factor X to Factor Xa is catalysed by Factor IXa.
30 Factor IXa is generated from Factor IX by the action of
31 Factor XIa, which in turn is generated by the action of
32 Factor XIIa on Factor XI. Factor XIIa is generated
33 from Factor XII by the action of Kallikrein. Factors

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1 VIIIa and Va are thought to act as cofactors in the
2 activation of Factors X and II, respectively.

3

4 Fibrin, as first formed from fibrinogen, is in the
5 loose form. Loose fibrin is converted to tight fibrin
6 by the action of Factor XIIIa, which crosslinks fibrin
7 molecules.

8

9 Activated protein C is an anticoagulant serine protease
10 generated in the area of clot formation by the action
11 of thrombin, in combination with thrombomodulin, on
12 protein C. Activated protein C regulates clot
13 formation by cleaving and inactivating the
14 pro-coagulant cofactors Va and VIIIa.

15

16 The term "enzyme involved in blood clotting" as used in
17 this specification therefore includes kallikrein
18 Factors XIIa, XIa, IXa, VIIa, Xa and thrombin (Factor
19 IIa), which are directly involved in the formation of
20 fibrin and activated protein C, which is involved in
21 the control of blood clotting. The most preferred
22 enzymes are Factor Xa and thrombin because they are
23 most immediately involved with fibrin formation.

24

25 Generation and activity of at least Factor Xa and
26 thrombin is tightly regulated to ensure that thrombus
27 generation is restricted to the site of the
28 thrombogenic stimulus. This localisation is achieved by
29 the combined operation of at least two control
30 mechanisms: the blood clotting enzymes function as
31 complexes intimately associated with the phospholipid
32 cellular membranes of platelets and endothelial cells
33 at the site of vascular injury (Mann, K. G., 1984, in:

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1 "Progress in Hemostasis and Thrombosis", 1 - 24, ed
2 Spaet, T. H. Grune and Stratton); and, free thrombin or
3 Factor Xa released from the thrombus site into the
4 circulation is rapidly inactivated by the action of
5 proteinase inhibitors such as anti-thrombin III.
6

7 Thus, the activity of the penultimate (Factor Xa) and
8 the final (thrombin) enzymes in the clotting cascade
9 are particularly well localised to the site of thrombus
10 generation and for this reason are preferred.

11 Thrombin has been found to remain associated with
12 thrombi and to bind non-covalently to fibrin. On
13 digestion of thrombi with plasmin, active thrombin is
14 liberated and is thought to contribute to the
15 reformation of thrombi and the re-occlusion of vessels
16 which commonly occurs following thrombolytic treatment
17 with plasminogen activators (Bloom A. L., 1962, Br. J.
18 Haematol., 82, 129; Francis et al, 1983, J. Lab. Clin. Med., 102, 220; Mirshahi et al, 1989, Blood 74, 1025).
19

20
21 For these reasons, it is preferred in certain
22 embodiments of the invention to produce fusion proteins
23 activatable by thrombin or Factor Xa thereby to create
24 a preferred class of thrombus-selective, fibrinolytic
25 proteins. The most preferred of these fusion proteins
26 regain the favourable properties of the parent
27 molecules upon cleavage and exhibit thrombus
28 selectivity by the novel property of being cleaved to
29 release the component proteins of the fusion protein at
30 the site of new thrombus formation by the action of one
31 of the enzymes involved in generation of the thrombus
32 and preferably localised there.
33

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1 Factor Xa (E.C.3.4.21.6) is a serine protease which
2 converts human prothrombin to thrombin by specific
3 cleavage of the Arg(273)-Thr(274) and Arg(322)-Ile(323)
4 peptide bonds (Mann *et al* 1981, Methods in Enzymology
5 80 286-302). In human prothrombin, the Arg(273)-
6 Thr(274) site is preceded by the tripeptide Ile-Glu-Gly
7 and the Arg(322)-Ile(323) site is preceded by the
8 tripeptide Ile-Asp-Gly. The structure required for
9 recognition by Factor Xa appears to be determined by
10 the local amino acid sequence preceding the cleavage
11 site (Magnusson *et al*, 1975, in: "Proteases and
12 Biological Control", 123-149, eds., Reich *et al*, Cold
13 Spring Harbor Laboratory, New York). Specificity for
14 the Ile-Glu-Gly-Arg and Ile-Asp-Gly-Arg sequence is not
15 absolute as Factor Xa has been found to cleave other
16 proteins, for example Factor VIII at positions 336,
17 372, 1689 and 1721, where the preceding amino acid
18 sequence differs significantly from this format (Eaton
19 *et al*, 1986 Biochemistry 25 505-512). As the principal
20 natural substrate for Factor Xa is prothrombin,
21 preferred recognition sequences are those in which
22 arginine and glycine occupy the P1 and P2 positions,
23 respectively, an acidic residue (aspartic or glutamic
24 acid) occupies the P3 position and isoleucine or
25 another small hydrophobic residue (such as alanine,
26 valine, leucine or methionine) occupies the P4
27 position. However, as Factor Xa can cleave sequences
28 which differ from this format, other sequences
29 cleavable by Factor Xa may be used in the invention, as
30 can other sequences cleavable by other enzymes of the
31 clotting cascade.

32

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1 In order to make fusion proteins which are cleavable by
2 these preferred enzymes, the amino acid sequence
3 linking the components of the fusion protein must be
4 recognised as a cleavage site for these preferred
5 enzymes. To make fusion proteins which are cleaved
6 by, for example, Factor Xa, an amino acid sequence
7 cleavable by Factor Xa may be used to link the two
8 components (that is, the first and second, and possibly
9 other, sequences) of the fusion protein. The sequence
10 Ile-Glu-Gly-Arg which is at one of the sites in
11 prothrombin cleaved by Factor Xa may be such a
12 sequence. Other possibilities would be sequences or
13 mimics of sequences cleaved by Factor Xa in other
14 proteins or peptides. DNA coding for the
15 Ile-Glu-Gly-Arg sequence as the carboxy-terminal part
16 of a cleavable linker as a protein production aid is
17 disclosed in UK Patent Application GB-A-2160206 but the
18 use of an Ile-Glu-Gly-Arg sequence for the purpose of
19 this invention is not disclosed in that specification.
20

21 Cleavage of fusion proteins by an enzyme of the
22 clotting cascade such as thrombin or Factor Xa can be
23 measured in a number of ways, for example by SDS-PAGE
24 analysis, and by assaying for the functions of one or
25 more of the cleavage products of the fusion protein.
26

27 Thrombin (E.C. 3.4.21.5) is a serine protease which
28 catalyses the proteolysis of a number of proteins
29 including fibrinogen (A alpha and B beta chains),
30 Factor XIII, Factor V, Factor VII, Factor VIII, protein
31 C and anti-thrombin III. The structure required for
32 recognition by thrombin appears to be partially
33 determined by the local amino acid sequence around the

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1 cleavage site but is also determined to a variable
2 extent by sequence(s) remote from the cleavage site.
3 For example, in the fibrinogen A alpha chain, residues
4 P2 (Val), P9 (Phe) and P10 (Asp) are crucial for
5 α -thrombin-catalysed cleavage at the Arg(16)-Gly(17)
6 peptide bond (Ni, F. et al 1989, Biochemistry 28
7 3082-3094). Comparative studies of several proteins
8 and peptides which are cleaved by thrombin has led to
9 the proposal that optimum cleavage sites for α -thrombin
10 may have the structure of (i) P4-P3-Pro-Arg-P1'-P2',
11 where each of P3 and P4 is independently a hydrophobic
12 amino acid (such as valine) and each of P1' and P2' is
13 independently a non-acidic amino acids, or (ii)
14 P2-Arg-P1' where P2 or P1' is glycine (Chang, J. 1985,
15 Eur. J. Biochem. 151 217-224). There are, however,
16 exceptions to these general structures which are
17 cleaved by thrombin and which may be used in the
18 invention.

19

20 To produce a fusion protein which could be cleaved by
21 thrombin, a linker sequence containing a site
22 recognised and cleaved by thrombin may be used. An
23 amino acid sequence such as that cleaved by thrombin in
24 the fibrinogen A alpha chain may be used. Other
25 possible sequences would include those involved in the
26 cleavage by thrombin of fibrinogen B beta, Factor XIII,
27 Factor V, Factor VII, Factor VIII, protein C,
28 anti-thrombin III and other proteins whose cleavage is
29 catalysed by thrombin. An example of a thrombin
30 cleavable linker may be the sequence Gly-Pro-Arg which
31 is identical to that found at positions 17-20 in
32 fibrinogen A alpha. This is not the principal thrombin
33 cleavage site in fibrinogen A alpha but thrombin can

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1 cleave the Arg(19)-Val(20) peptide bond. Another
2 suitable thrombin cleavable linker sequence is
3 Val-Glu-Leu-Gln-Gly-Val-Val-Pro-Arg which is identical
4 to that found in Factor XIII.

5

6 In a preferred embodiment the invention relates to
7 fusion proteins of streptokinase and/or hirudin linked
8 by peptide sequences which are cleaved by thrombin,
9 Factor Xa or other enzymes involved in blood clotting
10 to release products with fibrinolytic and/or anti-
11 thrombotic activity.

12

13 Fusion proteins in accordance with the invention may
14 contain other modifications (as compared to wild-type
15 counterparts of their components such as streptokinase
16 and hirudin) which may be one or more additions,
17 deletions or substitutions. An example of such a
18 modification would be streptokinase variants in which
19 inappropriate glycosylation during yeast expression was
20 prevented by substitution of sequences recognised as
21 glycosylation signals by yeast. Another example would
22 be the addition of an Arg-Gly-Asp-Xaa sequence, where
23 Xaa represents a variable amino acid such as Ser, to
24 the carboxy terminus of the fusion to enhance its
25 plasma lifetime.

26

27 Preferred features of fusion proteins within the scope
28 of the invention also apply, where appropriate, to
29 other compounds of the invention, mutatis mutandis.

30

31 Fusion proteins in accordance with the first aspect of
32 the invention can be synthesised by any convenient
33 route. According to a second aspect of the invention

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1 there is provided a process for the preparation of a
2 proteinaceous compound as described above, the process
3 comprising coupling successive amino acid residues
4 together and/or ligating oligopeptides. Although
5 proteins may in principle be synthesised wholly or
6 partly by chemical means, the route of choice will be
7 ribosomal translation, preferably in vivo, of a
8 corresponding nucleic acid sequence. The protein may
9 be glycosylated appropriately.

10

11 It is preferred to produce proteins in accordance with
12 the invention by using recombinant DNA technology. DNA
13 encoding each of the first and second sequences of the
14 fusion protein may be from a cDNA or genomic clone or
15 may be synthesised. Amino acid substitutions,
16 additions or deletions are preferably introduced by
17 site-specific mutagenesis. Suitable DNA sequences
18 encoding streptokinase and hirudin and other
19 polypeptide sequences useful in the scope of the
20 invention may be obtained by procedures familiar to
21 those having ordinary skill in genetic engineering.
22 For several proteins, it is a routine procedure to
23 obtain recombinant protein by inserting the coding
24 sequence into an expression vector and transfecting or
25 transforming the vector into a suitable host cell. A
26 suitable host may be a bacterium such as E. coli, a
27 eukaryotic microorganism such as yeast or a higher
28 eukaryotic cell.

29

30 According to a third aspect of the invention, there is
31 provided synthetic or recombinant nucleic acid coding
32 for a proteinaceous compound as described above. The
33 nucleic acid may be RNA or DNA. Preferred

1 characteristics of this aspect of the invention are as
2 for the first aspect.

3

4 According to a fourth aspect of the invention, there is
5 provided a process for the preparation of nucleic acid
6 in accordance with the third aspect, the process
7 comprising coupling successive nucleotides together
8 and/or ligating oligo- and/or polynucleotides.

9

10 Recombinant nucleic acid in accordance with the third
11 aspect of the invention may be in the form of a vector,
12 which may for example be a plasmid, cosmid or phage.
13 The vector may be adapted to transfect or transform
14 prokaryotic (for example bacterial) cells and/or
15 eukaryotic (for example yeast or mammalian) cells. A
16 vector will comprise a cloning site and usually at
17 least one marker gene. An expression vector will have
18 a promoter operatively linked to the sequence to be
19 inserted into the cloning site and, preferably, a
20 sequence enabling the protein product to be secreted.
21 Expression vectors and cloning vectors (which need not
22 be capable of expression) are included in the scope of
23 the invention.

24

25 It is to be understood that the term "vector" is used
26 in this specification in a functional sense and is not
27 to be construed as necessarily being limited to a
28 single nucleic acid molecule.

29

30 Using a vector, for example as described above, fusion
31 proteins in accordance with the invention may be
32 expressed and secreted into the cell culture medium in
33 a biologically active form without the need for any

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1 additional biological or chemical procedures. Suitable
2 cells or cell lines to be transformed may be mammalian
3 cells which grow in continuous culture and which can be
4 transfected or otherwise transformed by standard
5 techniques. Examples of suitable cells include Chinese
6 hamster ovary (CHO) cells, mouse myeloma cell lines
7 such as P3X63-Ag8.653, COS cells, HeLa cells, BHK
8 cells, melanoma cell lines such as the Bowes cell line,
9 mouse L cells, human hepatoma cell lines such as Hep
10 G2, mouse fibroblasts and mouse NIH 3T3 cells. Such
11 cells may be particularly appropriate for expression
12 when one or more of the protein sequences constituting
13 the fusion protein is of mammalian derivation, such as
14 tissue plasminogen activator (t-PA).

15

16 Yeast (for example Pichia pastoris or Saccharomyces
17 cerevisiae) or bacteria (for example Escherichia coli)
18 may be preferred for the expression of many of the
19 fusion proteins of the invention, as may insect cells
20 such as those which are Baculovirus-infected.

21

22 Compounds of the present invention may be used within
23 pharmaceutical compositions for the prevention or
24 treatment of thrombosis or other conditions where it is
25 desired to produce local fibrinolytic and/or
26 anticoagulant activity. Such conditions include
27 myocardial and cerebral infarction, arterial and venous
28 thrombosis, thromboembolism, post-surgical adhesions,
29 thrombophlebitis and diabetic vasculopathies.

30

31 According to a fifth aspect of the invention, there is
32 provided a pharmaceutical composition comprising one or
33 more compounds in accordance with the first aspect of

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1 the invention and a pharmaceutically or veterinarily
2 acceptable carrier. Such a composition may be adapted
3 for intravenous administration and may thus be sterile.
4 Examples of compositions in accordance with the
5 invention include preparations of sterile fusion
6 proteins in isotonic physiological saline and/or
7 buffer. The composition may include a local
8 anaesthetic to alleviate the pain of injection.
9 Compounds of the invention may be supplied in unit
10 dosage form, for example as a dry powder or water-free
11 concentrate in a hermetically sealed container such as
12 an ampoule or sachet indicating the quantity of
13 protein. Where a compound is to be administered by
14 infusion, it may be dispensed by means of an infusion
15 bottle containing sterile water for injections or
16 saline or a suitable buffer. Where it is to be
17 administered by injections, it may be dispensed with an
18 ampoule of water for injection, saline or a suitable
19 buffer. The infusible or injectable composition may be
20 made up by mixing the ingredients prior to
21 administration. Where it is to be administered as a
22 topical treatment, it may be dispensed in a suitable
23 base.

24

25 The quantity of material to be administered will depend
26 on the amount of fibrinolysis or inhibition of clotting
27 required, the required speed of action, the seriousness
28 of the thromboembolic position and the size of the
29 clot. The precise dose to be administered will, because
30 of the very nature of the condition which compounds of
31 the invention are intended to treat, be determined by
32 the physician. As a guideline, however, a patient
33 being treated for a mature thrombus will generally

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1 receive a daily dose of a fusion protein of from 0.01
2 to 10 mg/kg of body weight either by injection in for
3 example up to 5 doses or by infusion.

4

5 The invention may be used in a method for the treatment
6 or prophylaxis of thrombosis, comprising the
7 administration of an effective non-toxic amount of a
8 compound in accordance with the first aspect.
9 According to a further aspect of the invention, there
10 is therefore provided the use of a compound as
11 described above in the preparation of a thrombolytic
12 and/or anticoagulant agent.

13

14 The invention concerns especially the DNAs, the
15 vectors, the transformed host strains, the fusion
16 proteins and the process for the preparation thereof as
17 described in the examples.

18

19 The following examples of the invention are offered by
20 way of illustration, and not by way of limitation. The
21 examples refer to the accompanying drawings, in which:

22

23 Figure 1 shows schematically the arrangement of a
24 set of oligonucleotides used in the assembly of a
25 synthetic hirudin gene (Preparation 1);

26

27 Figure 2 shows a map of plasmid pSW6 (Preparation
28 2);

29

30

31 Figure 3 shows a map of plasmid pJK1 (Preparation
32 2);

33

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1 Figure 4 shows a map of plasmid pGC517 (Example
2 4);
3

4 Figure 5 shows a zymograph of E. coli strains
5 expressing streptokinase activity (Example 11);
6 and
7

8 Figure 6 shows a zymograph demonstrating cleavage
9 of a streptokinase-streptokinase fusion protein by
10 thrombin (Example 13).
11

12 Methodology
13

14 The techniques of genetic engineering and genetic
15 manipulation used in the manufacture of the genes
16 described and in their further manipulation for
17 construction of expression vectors are well known to
18 those skilled in the art. Descriptions of modern
19 techniques can be found in the laboratory manuals
20 "Current Protocols in Molecular Biology" , Volumes 7
21 and 2, edited by F. M. Ausubel *et al*, published by
22 Wiley-Interscience, New York and in "Molecular Cloning,
23 A Laboratory Manual" (second edition) edited by
24 Sambrook, Fritsch and Maniatis published by Cold
25 Spring Harbor Laboratories, New York. M13mpl8, M13mpl9
26 and pUC19 DNAs were purchased from Pharmacia Ltd.,
27 Midsummer Boulevard, Central Milton Keynes, Bucks, MK9
28 3HP, United Kingdom. Restriction endonucleases were
29 purchased either from Northumbria Biologicals Limited,
30 South Nelson Industrial Estate, Cramlington,
31 Northumberland, NE23 9HL, United Kingdom or from New
32 England Biolabs, 32 Tozer Road, Beverly, MA 01915-5510
33 USA. E. coli HW1110 (lacIq) is used as expression host

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1 in certain of the following examples: a suitable
2 commercially available alternative is JM109, available
3 from Northumbria Biologicals Ltd.

4

5 PREPARATION 1 - Construction of a Hirudin HV1 gene

6

7 A. Gene Design

8

9 A synthetic hirudin HV-1 gene was designed based on the
10 published amino acid sequence (Dodd J., et al FEBS
11 Letters 165 180 (1984)). Unique restriction
12 endonuclease target sites were incorporated to
13 facilitate subsequent genetic manipulation (see SEQ. ID
14 NO:1 in the Sequence Listings immediately before the
15 claims). The codons selected were those favoured by
16 either S. cerevisiae or E. coli and are thus suitable
17 for expression in either organism.

18

19 B. Gene Construction

20

21 The gene sequence was divided into 12 oligodeoxyribo-
22 nucleotides (see SEQ. ID NO:2) such that after
23 annealing each complementary pair 2 oligonucleotides,
24 they were left with cohesive ends either for or of 7
25 bases in length.

26

27 C. Oligonucleotide Synthesis

28

29 The oligonucleotides were synthesised by automated
30 phosphoramidite chemistry on an Applied Bio-Systems
31 380B DNA Synthesiser, using cyanoethyl
32 phosphoramidites. The methodology is now widely used
33 and has already been described (Beaucage, S.L. and

1 Caruthers, M.H. Tetrahedron Letters **24**, 245 (1981) and
2 Caruthers, M. H. Science **230**, 281-285 (1985)).

3

4 D. Gene Assembly

5

6 The oligonucleotides were kinased to provide them with
7 a 5' phosphate to allow their subsequent ligation. The
8 oligonucleotides were assembled as shown in Figure 1.

9

10 Kinasing of Oligomers

11

12 100 pmole of oligomer was dried down and resuspended in
13 20 µl kinase buffer (70 mM Tris, pH 7.6, 10 mM MgCl₂,
14 1 mM ATP, 0.2 mM spermidine, 0.5 mM dithiothreitol
15 (DTT)). T4 polynucleotide kinase (2 µl. 10 000 U/ml)
16 was added and the mixture was incubated at 37°C for 30
17 minutes. The kinase was then inactivated by heating at
18 70°C for 10 minutes.

19

20 Complementary pairs of kinased oligonucleotides were
21 annealed in pairs (90°C, 5 minutes, followed by slow
22 cooling at room temperature). The 6 paired oligomers
23 were then mixed together, incubated at 50°C for
24 5 minutes and allowed to cool. They were then ligated
25 overnight at 16°C with T4 DNA ligase. The strategy is
26 shown diagrammatically in Figure 1 (note
27 P = 5'-phosphate). To prevent possible multi-
28 merisation, oligomers designated BB2011 and BB2020
29 were not kinased. The sequences of the oligomers shown
30 in Figure 1 correspond to those given in SEQ.ID NO:2.

31

32 The ligation products were separated on a 2% low
33 gelling temperature agarose gel and the DNA fragment of

1 ca. 223 base pairs corresponding to the hirudin HV-1
2 gene was excised and extracted from the gel. The
3 purified fragment was then ligated to HindIII and EcoRI
4 treated pUC19 plasmid DNA. The transformation of E.
5 coli host strains was accomplished using standard
6 procedures. The strain used as a recipient in the
7 transformation of plasmid vectors was HW87 which has
8 the following genotype:

9
10 araD139(ara-leu)DELTA7697 (lacIPOZY)DELTA74 galU
11
12 galK hsdR rpsL srl recA56
13

14 The use of HW87 was not critical: any suitable
15 recipient strain could be used, for example, E. coli
16 AG1, which is available from Northumbria Biologicals
17 Ltd. The recombinant ligation products were
18 transformed into E. coli K12 host strain HW87 and
19 plated onto Luria-agar ampicillin (100 µg/ml) plates.
20 Twelve ampicillin-resistant colonies were picked and
21 used to prepare plasmid DNA for sequence analysis.
22 Double stranded dideoxy sequence analysis using a
23 universal sequencing primer BB22
24 (5'-CAGGGTTTCCCAGTCACG-3'), (SEQ ID NO:3)
25 complementary to the universal primer region of pUC19
26 was used to identify a correct clone pUC19 HV-1.
27 The pUC19 recombinant was used to construct an
28 expression vector.

29
30
31
32
33

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1 PREPARATION 2 - Construction of a Hirudin HV1
2 Expression Vector

3

4 An expression vector was designed to enable the
5 secretion of hirudin to the extracellular medium after
6 expression in S. cerevisiae. Secretion of hirudin is
7 desirable as this facilitates production of the protein
8 with an authentic N-terminus. It also eases
9 purification, limits intracellular proteolysis, reduces
10 potential toxic effects on the yeast host and allows
11 optimal protein folding and formation of native
12 disulphide bonds. Secretion of hirudin through the
13 yeast membrane was directed by fusion of hirudin to the
14 yeast mating type alpha-factor pre-pro-peptide (a
15 naturally secreted yeast peptide).

16

17 The yeast expression vector pSW6 (Figure 2) is based on
18 the 2 μ circle from S. cerevisiae. (pSW6 was deposited
19 in S. cerevisiae strain BJ2168 at The National
20 Collection of Industrial and Marine Bacteria Limited,
21 23 St. Machar Drive, Aberdeen, AB2 1RY, Scotland,
22 United Kingdom on 23rd October 1990 under Accession No.
23 NCIMB 40326.) pSW6 is a shuttle vector capable of
24 replication in both E. coli and S. cerevisiae and
25 contains an origin of DNA replication for both
26 organisms, the leu2 gene (a selectable marker for
27 plasmid maintenance in the yeast host) and the
28 ampicillin resistant locus for selection of plasmid
29 maintenance in E. coli. (The DNA sequence of the
30 vector has been determined; the E. coli sequences are
31 derived from the E. coli ColE1-based replicon pAT153.)
32 The full sequence is given as SEQ.ID:4. The ability
33 to passage this vector through E. coli greatly

1 facilitates its genetic manipulation and ease of
2 purification. pSW6 contains an α -factor
3 pre-pro-peptide gene fused in-frame to the gene for
4 epidermal growth factor (EGF). The expression of
5 this fusion is under the control of an efficient
6 galactose regulated promoter which contains hybrid DNA
7 sequences from the S. cerevisiae GAL 1-10 promoter and
8 the S. cerevisiae phosphoglycerate kinase (PGK)
9 promoter. Transcription of the EGF gene is terminated
10 in this vector by the natural yeast PGK terminator.
11 The EGF gene in pSW6 can be removed by digestion with
12 restriction endonucleases HindIII and BamHI. This
13 removes DNA encoding both EGF and 5 amino acids from
14 the C-terminus of the α -factor pro-peptide. Genes to
15 be inserted into the pSW6 expression vector must
16 therefore have the general composition: HindIII site -
17 α -factor adaptor - gene- BamHI site.

18

19 To rebuild the DNA encoding the amino acids at the
20 C-terminal end of the α -factor pro-peptide and to fuse
21 this to the synthetic hirudin gene, an oligonucleotide
22 adapter (5'-AGCTTGGATAAAAGA-3' (top strand, SEQ.ID:5),
23 5'-TCTTTTATCCA-3' (bottom strand, SEQ.ID:6)) containing
24 a HindIII site and codons encoding the Ser, Leu, Asp,
25 Lys and Arg from the C-terminal end of the α -factor
26 pro-peptide was constructed. The α -factor adaptor was
27 ligated to the synthetic HV-1 gene such that the
28 recombinant gene encoded an in-frame α -factor
29 pro-peptide fusion to hirudin. The pUC19 HV-1 plasmid
30 DNA of Preparation 1 was first cleaved with BspMI and
31 the overhanging ends were filled using DNA polymerase I
32 Klenow fragment to create a blunt-ended linear DNA
33 fragment. The linearised fragment was separated from

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1 uncut plasmid on a 1% low gelling temperature agarose
2 gel, excised and extracted from the agarose gel matrix,
3 then further treated with HindIII. The fragment was
4 then ligated to the alpha-factor adaptor described
5 above and annealed prior to ligation. The recombinant
6 ligation products were transformed into competent cells
7 of E. coli strain HW87 (Preparation 1). Ampicillin
8 resistant transformants were analysed by preparation of
9 plasmid DNA, digestion with HindIII and BamHI and
10 agarose gel electrophoresis. A correct recombinant
11 plasmid was called pJC80. The α-factor adaptor -
12 hirudin sequence was removed from pJC80 on a ca. 223 bp
13 HindIII-BamHI DNA fragment (SEQ.ID:7). The
14 fragment was purified on a low gelling temperature
15 agarose gel and ligated to HindIII and BamHI treated
16 pSW6 vector DNA. The recombinant ligation products
17 were transformed into competent cells of E. coli
18 strain HW87. Ampicillin resistant transformants were
19 screened by preparation of plasmid DNA, restriction
20 endonuclease analysis with HindIII and BamHI and
21 agarose gel electrophoresis. A clone with the correct
22 electrophoretic pattern pJK1 (Figure 3) was identified.
23 This plasmid is the basic vector used for wild-type
24 hirudin HV-1 expression and was used to derive certain
25 other yeast expression vectors as detailed in the
26 remaining preparations and examples.

27

28 PREPARATION 3 - Expression of Hirudin Synthetic Gene
29

30 Plasmid expression vector pJK1 of Preparation 2 was
31 transformed into yeast (S. cerevisiae) strain BJ2168
32 which has the following genotype: prc-1-407, prb1-1122
33 pep4-3 leu2 trpl ura3-52 cir+ using the method of

1 Sherman F. et al (Methods in Yeast Genetics, Cold
2 Spring Harbor Laboratory, (1986)). All yeast media
3 was as described by Sherman et al. Using 2 litre shake
4 flasks, cultures of yeast containing pJK1 were grown
5 in 1 litre batches of 0.67% synthetic complete medium,
6 yeast nitrogen base, with amino acids minus leucine and
7 1% glucose as a carbon source. After overnight growth
8 at 30°C, the cells were harvested by centrifugation at
9 3000 rpm for 10 minutes and resuspended in the same
10 synthetic complete medium except that 1% galactose and
11 0.2% glucose was used as the carbon source. This
12 induces gene expression from the hybrid PGK promoter.
13 Cells were grown in the induction medium for 3 days.
14 After this period, the supernatant was harvested and
15 assayed for hirudin activity as described in Example 2,
16 Section D, below.

17

18 EXAMPLE 1 - Construction of a Hirudin-IEGR-Hirudin
19 Fusion Gene and a Vector for its Expression

20

21 A factor Xa-cleavable hirudin fusion protein molecule
22 has been engineered in which two full length hirudin
23 molecules are joined by the peptide linker sequence
24 Ile Glu Gly Arg (See SEQ.ID NO:8). The molecule is
25 designed to be activatable by factor Xa cleavage.
26 The strategy for construction of the
27 hirudin-IEGR-hirudin gene is detailed below.

28

29 A gene encoding the hirudin-IEGR-hirudin molecule was
30 constructed by oligonucleotide directed mutagenesis
31 and molecular cloning. Mutagenesis was carried out
32 according to the method of Kunkel et al., Methods in
33 Enzymology, 154, 367-382 (1987). Host strains are
34 described below.

1 E. coli strains

2

3 RZ1032 is a derivative of E. coli that lacks two
4 enzymes of DNA metabolism: (a) dUTPase (dut), the lack
5 of which results in a high concentration of
6 intracellular dUTP, and (b) uracil N-glycosylase (ung)
7 which is responsible for removing mis-incorporated
8 uracils from DNA (Kunkel et al., loc. cit.). A
9 suitable alternative strain is CJ236, available from
10 Bio-Rad Laboratories, Watford WD1 8RP, United Kingdom.
11 The principal benefit is that these mutations lead to
12 a higher frequency of mutants in site directed
13 mutagenesis. RZ1032 has the following genotype:

14

15 HfrKL16PO/45[lysA961-62], dut1, ung1, thi1,
16 recA, Zbd-279::Tn10, supE44

17

18 JM103 is a standard recipient strain for manipulations
19 involving M13 based vectors. The genotype of JM103 is
20 DELTA (lac-pro), thi, supE, strA, endA, sbcB15, hspR4,
21 F' traD36, proAB, lacIq, lacZDELTAM15. A suitable
22 commercially available alternative E. coli strain is
23 E. coli JM109, available from Northumbria Biologicals
24 Ltd.

25

26 Mutagenesis

27

28 Prior to mutagenesis it was necessary to juxtapose two
29 adjacent hirudin genes in an M13 mutagenesis vector.
30 This was accomplished as described below. pJK1
31 vector DNA of Preparation 2 was prepared and an
32 aliquot treated with restriction endonucleases BglII
33 and BamHI, a ca. 466 bp BglII-BamHI DNA fragment from

1 this digestion was gel purified and ligated to BamHI
2 treated and phosphatased pJC80 vector DNA of
3 Preparation 2. The recombinant ligation products were
4 transformed into competent cells of E. coli strain
5 HW87 (Preparation 1). Ampicillin (100 µg/ml) resistant
6 clones were analysed by plasmid DNA preparation,
7 restriction endonuclease digestion and gel
8 electrophoresis. Clones with inserts in the desired
9 orientation were identified after digestion with KpnI
10 which released a DNA fragment of ca. 465bp in length.
11 (The products of KpnI digestion were analysed on an
12 agarose gel.) One of the correct clones, pJK002, was
13 used for the remaining constructions, this vector
14 contains a ca. 465 bp KpnI DNA fragment which encodes a
15 C-terminal portion of a first hirudin gene, a
16 complete α-factor pre-pro-peptide sequence and the
17 N-terminal portion of a second hirudin gene. In order
18 to delete the α-factor pre-pro-peptide sequence and to
19 insert DNA encoding a factor Xa-cleavable amino acid
20 linker sequence (IEGR), the ca. 465 bp KpnI DNA
21 fragment was transferred into a bacteriophage
22 mutagenesis vector M13mp18. Plasmid DNA of pJK002 was
23 prepared and a portion was digested with KpnI. The ca.
24 465 bp KpnI DNA fragment from pJK002 was gel purified
25 and ligated to KpnI treated and phosphatased M13mp18.
26 The recombinant ligation products were transfected
27 into competent cells of E. coli strain JM103. Single
28 stranded DNAs from putative recombinant phage plaques
29 were prepared and analysed by dideoxy sequence analysis
30 using the M13 universal sequencing primer (SEQ. ID NO:
31 10; see below). A clone pGC609 containing the KpnI
32 fragment in the correct orientation was identified.

1 The α -factor pre-pro-peptide sequence between the two
2 hirudin sequences of pGC609 was deleted and the DNA
3 encoding the Factor Xa-cleavable amino acid linker
4 (IEGR) inserted by site directed mutagenesis. Single
5 stranded DNA of pGC609 was prepared from E. coli
6 strain RZ1032 and was used as a template for
7 mutagenesis with a 46mer oligonucleotide BB2988:
8 (5'-CAGTCGGTGTAAACAACTCTTCCTCGATCTGCAGATATTCTTCTG-3')
9 (SEQ. ID NO:9). Single stranded DNAs were prepared
10 from putative mutant plaques and were analysed by
11 dideoxy DNA sequence analysis using an M13 universal
12 sequencing primer (United States Biochemical
13 Corporation. P.O. Box 22400, Cleveland, Ohio 44122.
14 USA. Product No. 70763 5'-GTTTTCCCAAGTCACGAC-3'), (SEQ.
15 ID NO:10). A correct clone, pGC610, was identified.
16 To construct the full length hirudin-IEGR-hirudin gene
17 the central core of the fusion molecule encoded on the
18 ca. 210 bp KpnI fragment of pGC610 was cloned into the
19 KpnI site of pJC80 of Preparation 2. Replicative form
20 DNA of pGC610 was prepared and digested with KpnI. The
21 ca. 210 bp KpnI DNA fragment encoding the central core
22 of the hirudin-IEGR-hirudin protein was gel purified
23 and ligated to KpnI treated and phosphatased pJC80 of
24 Preparation 2. The recombinant ligation products were
25 transformed into competent cells of E. coli strain HW87
26 (Preparation 1). Ampicillin (100 μ g/ml) resistant
27 transformants were analysed by preparation of plasmid
28 DNA, restriction endonuclease digestion with PstI and
29 agarose gel electrophoresis. A clone with the correct
30 electrophoretic pattern pDB1 was identified as
31 containing a ca. 210 bp DNA fragment after PstI
32 digestion.

33

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1 To create a vector for the expression of the factor
2 Xa-cleavable hirudin-IEGR-hirudin fusion protein the
3 gene was cloned into the yeast expression vector pSW6
4 of Preparation 2. Plasmid DNA of pDB1 was treated
5 with HindIII and BamHI and the ca. 420 bp HindIII-BamHI
6 DNA fragment containing the factor Xa-cleavable
7 hirudin-IEGR-hirudin gene was gel purified and ligated
8 to HindIII and BamHI treated pSW6 DNA of Preparation 2.
9 The recombinant ligation products were transformed
10 into competent cells of E. coli strain HW87.
11 Ampicillin (100 µg/ml) resistant transformants were
12 screened by preparation of plasmid DNA, restriction
13 endonuclease analysis with HindIII and BamHI and
14 agarose gel electrophoresis. A clone with the correct
15 electrophoretic pattern pDB2 was identified. pDB2
16 contained the hirudin-IEGR-hirudin gene fused in frame
17 to the yeast α-factor pre-pro-peptide sequence. pDB2
18 plasmid DNA was prepared and used to transform yeast
19 strain BJ2168 (Preparation 3) according to the method
20 of Sherman F. et al (Methods in Yeast Genetics, Cold
21 Spring Harbor Laboratory, New York (1986)).
22

23 EXAMPLE 2 - Purification of Hirudin and
24 Hirudin-IEGR-Hirudin

25
26 The procedure of Preparation 3 was generally followed
27 for the expression of hirudin and hirudin-IEGR-hirudin
28 proteins. Hirudin and hirudin-IEGR-hirudin are
29 purified from yeast culture broth. Cells were first
30 removed by centrifugation at 3000 rpm for 10 minutes.
31 The supernatant was then assayed for biological
32 activity using a chromogenic assay (see below, section
33 D). Production levels from shake flask cultures

1 were routinely between 10-15 mg/litre of culture. The
2 hirudin protein was purified by preparative HPLC
3 (DYNAMAX (Trade Mark) C18, 300 angstroms). The column
4 was first equilibrated in 15% acetonitrile, 0.1%
5 trifluoro acetic acid. Then 2.5-3 mg of hirudin
6 activity as determined by chromogenic assay (section
7 D) was loaded onto the column. The protein was
8 eluted using a 15-40% acetonitrile gradient at 3
9 ml/minute over 25 min. The purity of the isolated
10 protein was assessed by analytical HPLC (VYDAC (Trade
11 Mark) C18 reverse phase), N-terminal sequence analysis
12 and mono Q FPLC as described below.
13

14 A. Assessing Purity by Analytical HPLC

15
16 Samples were analysed on a VYDAC (Trade Mark) C18
17 column (15 x 0.46cm, particle size 5 micron)
18 equilibrated with 10% acetonitrile, 0.1% trifluoroacetic
19 acid (TFA). Purified protein (20 µg) was loaded in
20 10% acetonitrile, 0.1% TFA. Protein was eluted at a
21 flow rate of 1ml/minute using an acetonitrile gradient
22 from 10-40% in 0.1% TFA over 30 minutes. The eluted
23 protein sample was monitored by absorbance at 280 nm.
24

25 B. Analysis of Purity by Mono Q FPLC

26
27 Samples were analysed on a Mono Q FPLC column
28 (5 x 0.5cm, Pharmacia) equilibrated in 20 mM Tris.HCl
29 pH 7.5. Approximately 15 µg of lyophilised protein
30 was reconstituted in 1ml 20mM Tris.HCl pH 7.5 and
31 loaded onto the column. Protein was eluted using a
32 gradient of 0-250mM NaCl in 20 mM Tris.HCl buffer
33 (pH 7.5) at a flow rate of 1ml/minute over 30 minutes.

1 C. N-terminal Sequence Analysis

2

3 N-terminal sequence analysis was performed by
4 automated Edman degradation using an Applied Biosystems
5 Protein Sequencer, model 471 A (Applied Biosystems,
6 Foster City, California).

7

8 Purified material that was greater than 95% pure, was
9 dried down in a SPEEDIVAC (trade mark of Savant
10 Instruments Inc. Hicksville, N.Y. U.S.A.) and
11 reconstituted in 0.5 ml of 0.9% (w/v) saline for assay.

12

13 D. Hirudin Anti-thrombin Chromogenic Activity Assay

14

15 The ability of hirudin and molecules containing hirudin
16 to inhibit the thrombin catalysed hydrolysis of the
17 chromogenic substrate tosyl-Gly-Pro-Arg-p-nitroanilide
18 (CHROMOZYM TH (trade mark of Boehringer-Mannheim)) was
19 used as an assay to determine their anti-thrombin
20 activity. Protein samples (50 µl) diluted in 0.1M
21 Tris.HCl pH8.5, 0.15 M NaCl, 0.1% (w/v) PEG 6000 were
22 mixed with 50 µl human thrombin (Sigma, 0.8 U/ml in the
23 above buffer) and 50 µl CHROMOZYM TH (2.5mM in water)
24 in 96 well plates (Costar). The plates were incubated
25 at room temperature for 30 minutes. The reaction was
26 terminated by adding 50 µl 0.5 M acetic acid and the
27 absorbance read at 405 nm using an automatic plate
28 reader (Dynatech). Quantitation was performed by
29 comparison with a standard hirudin preparation
30 (recombinant [Lys-47]-HV-2 purchased from Sigma: Sigma
31 Chemical Co. Ltd, Fancy Road, Poole, Dorset BH11 7TG,
32 United Kingdom).

33

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1 EXAMPLE 3 - Cleavage and Activation of Hirudin-IEGR-
2 Hirudin Fusion Protein

3

4 Purified hirudin-IEGR-hirudin fusion protein was
5 incubated with Factor Xa. The reaction was performed
6 at 37°C in a total volume of 150 µl of 0.1M Tris.HCl
7 buffer pH 7.8 and contained 2.06 nmol fusion protein
8 and 0.4 nmol Factor Xa. Analysis of the reaction
9 mixture by sodium dodecyl sulphate-polyacrylamide gel
10 electro- phoresis (SDS-PAGE) demonstrated cleavage to
11 products of a similar size to native hirudin. Reverse
12 phase HPLC analysis of the cleavage reaction as in
13 Example 2, section A, demonstrated the appearance of
14 two new species with retention times (RT) of 17 and 20
15 minutes compared to 22 minutes for the intact fusion
16 protein.

17

18 Measurements of specific activity were made on the
19 products isolated from a cleavage reaction. Using a
20 chromogenic assay according to the method of Example
21 2, section D, to measure hirudin activity in
22 anti-thrombin units and A 280 nm to determine protein
23 concentration, the following results were obtained:
24 product RT 17 min., 6125 U/mg; product RT 20 min.,
25 5226 U/mg; intact hirudin-IEGR-hirudin, RT 22 min.,
26 2588 U/mg. Cleavage therefore produces an approximate
27 2-fold increase in specific activity, with the products
28 displaying similar values to that recorded for a
29 recombinant hirudin sample (6600 U/mg) as measured
30 according to the method of Example 2, section D.

31

32 Purified cleavage products and the intact fusion
33 protein were subjected to N-terminal sequence analysis.

1 In each case the sequence obtained was identical to
2 that of native hirudin (HV1), (VVYTD).

3

4 It has thus been demonstrated that the
5 hirudin-IEGR-hirudin fusion protein can be cleaved
6 by Factor Xa to produce two products with hirudin
7 activated. Cleavage of the fusion protein is
8 accompanied by activation as the products of
9 cleavage have approximately double the specific
10 activity of the fusion protein.

11

12 PREPARATION 4 - Isolation of a streptokinase gene

13

14 Streptokinase is secreted by Lancefield's Group C
15 streptococci and cloning of the streptokinase gene from
16 Streptococcus equisimilis strain H46A has been
17 described (Malke,H. and J.J. Ferretti, P.N.A.S. 81
18 3557-3561 (1984)). The nucleotide sequence of the
19 cloned gene has been determined (Malke, H., Roe, B.
20 and J.J. Ferretti, Gene 34 357-362 (1985)). A gene
21 encoding streptokinase has been cloned from
22 S. equisimilis (ATCC 9542 or ATCC 10009) for use in the
23 current invention. Methods that can be used to
24 isolate genes are well documented and the procedure
25 used to isolate the streptokinase gene is summarized in
26 the following protocol.

27

28 1. DNA was prepared either from Streptococcus
29 equisimilis (Lancefield's Group C) ATCC 10009 or from
30 ATCC 9542 grown in brain-heart infusion medium
31 (Difco-Bacto Laboratories, PO Box 14B, Central Avenue,
32 E. Mosely, Surrey KT8 OSE, England) as standing
33 cultures. Chromosomal DNA was isolated from

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1 approximately 1.5 ml of cells at a density of 1×10^{11}
2 cells/ml. The cells were harvested and washed in 1ml
3 buffer (0.1M potassium phosphate pH 6.2). The pellet
4 was resuspended in 400 μ l of the same buffer and 500
5 units of mutanolysin (Sigma Chemical Company Ltd, Fancy
6 Road, Poole, Dorset BH17 7TG, UK) in 100 μ l volume was
7 added. This mix was incubated at 37°C for 1 hour. The
8 cells were harvested by centrifugation and again washed
9 in buffer. The cells were resuspended in 500 μ l of a
10 solution containing 50mM glucose, 10mM EDTA and 25mM
11 Tris HCl pH 8.0 and incubated at 37°C for approximately
12 1 hour with the mix being shaken gently to prevent the
13 cells settling. A 500 μ l aliquot of a solution
14 containing 0.4% SDS and proteinase K (100 μ g/ml) (Sigma
15 Chemical Company Ltd) was added and the mix was
16 incubated at 37°C for 1 hour until it became viscous
17 and clear. The mix was then extracted three times with
18 phenol equilibrated with TE buffer (10mM Tris HCl, 1mM
19 EDTA pH 8.0). The aqueous phase was removed into an
20 eppendorf tube, sodium acetate added to a final
21 concentration of 0.3M and 2.5 volumes of ethanol added.
22 The mix was incubated at -70°C for 1 hour to
23 precipitate the DNA. The DNA was pelleted by
24 centrifugation, washed with 70% ethanol and then
25 resuspended in 200 μ l TE buffer.

26

27 2. The Polymerase Chain Reaction (PCR) was used to
28 amplify the streptokinase sequence (Saiki R. *et al*
29 Science, 239, 487-491 (1988)). Two primers were
30 designed based on the published streptokinase
31 sequences. The primer encoding the antisense strand at
32 the 3' end of the gene was a 40mer BB1888
33 (5'GTTCATGGATCCTTATTGTCGTTAGGGTTATCAGGTATA 3'), (SEQ.

1 ID NO:11) which also encoded a BamHI site. The primer
2 encoding the sense strand at the 5' end of the gene
3 encoded an EcoRI site in addition to the streptokinase
4 sequence and was the 40mer BB1887
5 (5'TCAAGTGAATTCATGAAAAATTACTTATCTTTGGGATGT 3'), (SEQ
6 ID NO:12). Forty cycles of PCR were performed with the
7 denaturation step at 95°C for 2 minutes, followed by
8 annealing of the primers for 3 minutes at 55°C and
9 extension at 70°C for 4.5 minutes. A sample of the
10 reaction product was analysed on a 0.8% agarose gel.
11 A single amplified DNA fragment at c.a. 1.3 kB, which
12 corresponds to the expected size of the streptokinase
13 gene, was observed.

14

15 3. A 30μl sample of the product was digested with the
16 restriction endonucleases EcoRI and BamHI, analysed on
17 a low gelling temperature agarose gel and the
18 c.a. 1.3 kb DNA fragment was isolated from the gel.
19 The band was extracted from the gel and ligated into
20 the plasmid pUC19 which had been cleaved with EcoRI and
21 BamHI to form the plasmid pUC19SK.

22

23 The entire ca. 1330 bp EcoRI-BamHI fragment from
24 pUC19SK was sequenced by dideoxy sequence analysis.
25 To facilitate the sequencing, The EcoRI-BamHI DNA
26 fragment of pUC19SK was transferred to M13 sequencing
27 vectors mp18 and mp19 in two halves. A ca. 830 bp
28 EcoRI-HindIII DNA fragment was separately transferred
29 into EcoRI and HindIII treated M13mp18 and M13mp19.
30 The products from these two ligation events were
31 separately transfected into competent cells of E. coli
32 host JM103. Single stranded DNA was prepared and used
33 for dideoxy sequence analysis using the primers listed

1 in SEQ ID NO: 13 and SEQ ID NO: 10. A ca. 490 bp
2 HindIII-BamHI fragment was gel purified after
3 treatment of pUC19SK with HindIII and BamHI. This DNA
4 fragment was separately ligated to M13mp18 and M13mp19
5 which had been treated with HindIII and BamHI. The
6 products of these two ligation was transfected into
7 competent cells of E. coli host JM103. Single stranded
8 DNA was prepared and used for dideoxy sequence analysis
9 with the primers shown in SEQ ID NO:13 and SEQ ID
10 NO: 10. The entire sequence of the EcoRI-BamHI PCR
11 derived DNA fragment is shown in SEQ ID NO:14.
12

13 EXAMPLE 4 - Construction of Streptokinase Expression
14 Vectors

15

16 A number of alternative streptokinase expression
17 vectors have been constructed for expression in either
18 yeast S. cerevisiae or E. coli K12.

19

20 1) Vectors for secretion to the periplasm of E. coli
21 K12

22

23 Two vectors were designed to enable the secretion of
24 streptokinase to the periplasmic space after expression
25 in E. coli K12. Secretion of streptokinase is
26 desirable to facilitate production of protein with an
27 authentic N-terminus, to ease purification, to reduce
28 potential toxic effects and to limit intracellular
29 proteolysis. Secretion of streptokinase through
30 the E. coli cytoplasmic cell membrane was directed by
31 either the streptokinase signal peptide or the E. coli
32 major outer membrane protein A (OmpA) signal peptide
33 (OmpAL).

1 A. Secretion using the streptokinase leader

2

3 The streptokinase gene of Preparation 4 was
4 transferred into the E. coli expression vector pGC517
5 (Figure 4). pGC517 contains the regulatable ptac
6 promoter, a ribosome binding site and a synthetic
7 transcriptional terminator. pGC517 was deposited in
8 E. coli K12 at The National Collection of Industrial
9 and Marine Bacteria Limited, 23 St. Machar Drive,
10 Aberdeen, AB2 1RY, Scotland, United Kingdom on 5th
11 December 1990 under Accession No. NCIMB 40343. Genes
12 can be cloned into the expression site of pGC517 on
13 NdeI-BamHI DNA fragments. It was necessary to
14 engineer a NdeI site into the 5' end of the
15 streptokinase gene to enable subsequent cloning into
16 pGC517. The NdeI site was introduced by site-directed
17 mutagenesis. To construct the vector for the site
18 directed mutagenesis, plasmid DNA of vector pUC19SK of
19 Preparation 4 was prepared and digested with EcoRI and
20 BamHI and the ca. 1.3 Kb EcoRI-BamHI DNA fragment was
21 gel purified and ligated to M13mp18 treated with
22 EcoRI and BamHI. Recombinant ligation products were
23 transfected into competent cells of E. coli strain
24 JM103 (Example 1). Single stranded DNA was prepared
25 from the putative recombinant plaques and analysed by
26 dideoxy sequence analysis using the M13 universal
27 sequencing primer (SEQ ID NO: 10 of Example 1). One of
28 the correct recombinant phages was called pGC611.
29 Single stranded DNA of phage pGC611 was prepared from
30 E. coli strain RZ1032 (Example 1) and used as a
31 template for mutagenesis. An NdeI restriction site was
32 introduced by site-directed mutagenesis at the 5' end
33 of the streptokinase gene such that the NdeI site

1 overlapped the streptokinase initiation codon. The
2 mutagenesis was performed using a 26-mer BB2175
3 (5'-GATAAGTAATTTTCATATGAATTG-3'), (SEQ ID NO:15).
4 Single stranded DNAs were prepared from putative
5 mutant plaques and were screened by dideoxy sequence
6 analysis using the 18mer sequencing primer BB2358
7 (5'-CATGAGCAGGTCGTGATG-3'), (SEQ ID NO:16) and a
8 correct clone pGC612 was identified.
9

10 To construct an expression vector, the streptokinase
11 gene carrying the newly introduced NdeI site, was
12 cloned into the pGC517 expression vector. Replicative
13 form DNA was prepared from pGC612 and was digested
14 with NdeI and BamHI and the ca. 1.3 kb NdeI-BamHI DNA
15 fragment was gel purified. This fragment was then
16 ligated to NdeI and BamHI treated pGC517 DNA. The
17 recombinant ligation products were transformed into
18 competent cells of E. coli strain JM103. Ampicillin
19 (100 µg/ml) resistant transformants were analysed by
20 plasmid DNA preparation, restriction endonuclease
21 digestion with BglII and BamHI and agarose gel
22 electrophoresis. One of the correct clones, pKJ2, was
23 verified by dideoxy sequence analysis using the
24 sequencing primer BB2358. This vector contains the
25 entire streptokinase gene including the sequences
26 encoding the streptokinase signal peptide leader
27 region and was used for the expression of streptokinase
28 in E. coli.
29

30 B. Secretion using the E. coli OmpA leader
31

32 As an alternative secretion signal, a DNA sequence
33 encoding the major outer membrane protein A (OmpA)

1 signal peptide (OmpAL) was fused to the DNA sequence
2 encoding the mature streptokinase protein; see SEQ ID
3 NO:17. A DNA fragment encoding streptokinase was
4 obtained by preparing pUC19SK vector DNA, treating the
5 DNA with EcoRI and filling-in the overhanging single
6 stranded DNA ends with DNA polymerase I Klenow
7 fragment to create a blunt-ended linear DNA fragment.
8 The fragment was next digested with BamHI and the ca.
9 1.3 kb blunt-ended-BamHI DNA fragment containing the
10 streptokinase gene was gel-purified. The DNA sequence
11 encoding OmpAL is available on an expression vector
12 pSD15. The pSD15 vector contains a gene encoding an
13 insulin like growth factor II gene (IGF-II) fused to
14 the OmpAL signal sequence. pSD15 was deposited in
15 E. coli K12 at The National Collection of Industrial
16 and Marine Bacteria Limited, 23 St. Machar Drive,
17 Aberdeen, AB2 1RY, Scotland, United Kingdom on 5th
18 December 1990 under Accession No. NCIMB 40342. In
19 order to use pSD15 as a vector to provide the OmpAL DNA
20 sequence, pSD15 vector DNA was treated with NheI, the
21 single stranded DNA overhanging ends were filled-in
22 with DNA polymerase I Klenow fragment to create a
23 blunt-ended linear DNA fragment. The linear DNA
24 fragment was next digested with BamHI which removed
25 ca. 123 bp from the 3' end of the IGF-II gene in pSD15.
26 After restriction endonuclease digestion the cleaved
27 linear DNA fragment was treated with phosphatase, to
28 prevent recircularisation of any partially cut vector
29 DNA and was gel purified then ligated to the
30 blunt-ended-BamHI DNA fragment containing the
31 streptokinase gene. The ligated mixture was
32 transformed into competent cells of E. coli strain HW87
33 (Preparation 1). Ampicillin (100 µg/ml) resistant

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1 recombinants carrying the streptokinase gene were
2 characterised by preparation of plasmid DNA,
3 restriction endonuclease analysis with BglII and
4 HindIII and agarose gel electrophoresis. A construct
5 of the correct electrophoretic pattern was called pKJ1.
6 Vector pKJ1 contains the DNA encoding OmpAL and
7 streptokinase separated by a region of DNA not required
8 in further constructs. The sequence of the insert DNA
9 in pKJ1 was confirmed by dideoxy sequence
10 analysis with a 44-mer oligonucleotide BB58
11 (5'-AGCTCGTAGACACTCTGCAGTTCTGGTGGCTTC-3')
12 SEQ ID NO:18. In order to create a DNA template for
13 the deletion loopout mutagenesis of the unwanted DNA
14 sequence, the BglII to HindIII DNA fragment from pKJ1
15 was cloned into a vector M13mp19. pKJ1 vector DNA
16 was treated with BglII and HindIII to produce a
17 ca. 1026 bp DNA fragment, which was gel purified and
18 ligated into the polylinker region of M13mp19
19 replicative form DNA treated with BamHI and HindIII.
20 Ligation products were transfected into competent
21 cells of E. coli strain JM103. Single stranded DNAs
22 were prepared from putative recombinant plaques and a
23 correct clone (pGC600) identified by dideoxy sequence
24 analysis using the M13 universal sequencing primer (SEQ
25 ID NO:10, Example 1).

26
27 Mutagenesis on template pGC600 was performed using a
28 30-mer oligonucleotide mutagenesis primer
29 BB2658 (5'-ACCGTAGCGCAGGCCATTGCTGGACCTGAG-3') SEQ ID
30 NO:19. Single stranded DNAs were prepared from
31 putative mutant plaques and a clone, pGC601, containing
32 the required deletion was identified using dideoxy
33 sequence analysis with the M13 universal sequencing

1 primer (SEQ ID NO: 10). pGC601 contains part of the
2 OmpAL-streptokinase fusion required for the secretion
3 of streptokinase from this signal peptide in E. coli,
4 but DNA encoding the C-terminal portion of
5 streptokinase is absent. In order to reconstruct the
6 streptokinase gene, replicative form DNA from pGC601
7 was digested with restriction enzymes NdeI and HindIII
8 and the ca. 810 bp NdeI-HindIII DNA fragment containing
9 the DNA sequences encoding OmpAL leader peptide
10 sequence fused to the N-terminal portion of
11 streptokinase was gel purified. pJK2 vector DNA was
12 treated with restriction enzymes NdeI and HindIII
13 followed by treatment with phosphatase and the ca. 3620
14 bp NdeI-HindIII vector DNA fragment containing the
15 essential vector sequences and the C-terminal portion
16 of the streptokinase gene was gel purified. The
17 ca. 810 bp NdeI-HindIII (pGC601) and ca. 3620
18 NdeI-HindIII (pJK2) gel purified DNA fragments were
19 ligated together and the recombinant ligation products
20 were transformed into competent cells of E. coli
21 strain HW1110 (lacIq). The lacIq mutation in this
22 strain enhances repression of transcription from the
23 tac promoter. Any other lacIq strain, for example
24 JM103 could be used instead. The ampicillin resistant
25 transformants were screened by preparation of plasmid
26 DNA followed by restriction endonuclease analysis using
27 NdeI and HindIII. Agarose gel electrophoresis of
28 digestion products was used to identify a correct clone
29 which was called pLGC1. The pLGC1 construct was
30 verified by dideoxy sequence analysis using a 17-mer
31 oligonucleotide BB2753 (5'-GACACCAACCGTATCAT-3'), (SEQ
32 ID NO: 20) to sequence through the BamHI site and
33 primer BB3510 (5'-CACTATCAGTAGCAAAT-3'), (SEQ ID NO: 21)

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1 to sequence through the sequence encoding the OmpA
2 leader.

3

4 2) Intracellular Expression in E. coli

5

6 As streptokinase contains no disulphide bonds there is
7 no requirement for secretion to encourage native
8 protein folding and although streptokinase is
9 naturally secreted, intracellular expression offers
10 several potential advantages such as high yield and
11 inclusion body formation which may facilitate
12 purification. As an alternative production route,
13 an expression vector was designed for intracellular
14 production of streptokinase in E. coli. DNA encoding
15 the amino acids 2 to 21 of the OmpAL signal peptide
16 sequence which was fused to mature streptokinase in
17 pGC601 were deleted by loopout site directed
18 mutagenesis using single stranded DNA of pGC601
19 with a 31-mer mutagenesis oligonucleotide
20 BB3802 (5'-GAAATACTTACATATGATTGCTGGACCTGAG-3'), (SEQ
21 ID NO:22). In addition to deleting the OmpAL
22 signal peptide coding sequence, BB3802 fused the
23 methionine codon (ATG) of the OmpAL signal peptide
24 sequence to the first codon of mature streptokinase
25 to create the 5' end of gene encoding a
26 Methionyl-streptokinase fusion protein (see SEQ ID
27 NO:23). The ATG codon was used to allow
28 initiation of translation at the correct position.
29 Single stranded DNA was prepared from putative mutant
30 plaques and a clone containing the desired mutation,
31 pGC602 was identified using dideoxy sequence
32 analysis with the M13 universal sequencing primer
33 (SEQ ID NO:10). The C-terminal portion of the

1 streptokinase gene is missing in pGC602. In
2 order to reconstruct the intact mature streptokinase
3 coding sequence, replicative form DNA from pGC602 was
4 digested with restriction enzymes NdeI and HindIII and
5 the ca. 755 bp NdeI-HindIII DNA fragment encoding
6 the N-terminal portion of the Methionyl-streptokinase
7 protein was gel purified and ligated to the gel
8 purified ca. 3620 bp NdeI-HindIII pLGC2 vector DNA
9 fragment described in Example 6 below. The recombinant
10 ligation mixture was transformed into competent cells
11 of E. coli strain HW1110 (lacIq). Ampicillin
12 (100 µg/ml) resistant transformants were screened
13 by plasmid DNA preparation, restriction endonuclease
14 digestion and agarose gel electrophoresis. A clone ,
15 pGC603, with the correct electrophoretic pattern after
16 NdeI and HindIII digestion, was identified. Vector
17 pGC603 was used for the intracellular expression of
18 Methionyl-streptokinase in E. coli strain HW1110.
19

20 3) Construction of Expression Vectors for the
21 Secretion of Streptokinase from the Yeast
22 S. cerevisiae

23

24 Expression vectors were designed to enable the
25 secretion of streptokinase to the extracellular
26 medium after expression in S. cerevisiae. Secretion
27 of streptokinase is desirable to facilitate production
28 of protein with an authentic N-terminus, to ease
29 purification, to limit intracellular proteolysis
30 and to reduce potential toxic effects on the yeast
31 host. Secretion of streptokinase through the
32 yeast membrane was directed by either the natural
33 streptokinase signal peptide or by fusion of

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1 mature streptokinase to the yeast mating type
2 alpha-factor pre-pro-peptide (a naturally secreted
3 yeast peptide) see SEQ ID NO:24.
4

5 A) Secretion of Streptokinase using the Streptokinase
6 Signal Peptide
7

8 The streptokinase gene with its natural signal
9 peptide was cloned into the yeast expression
10 vector pSW6 to allow its expression in the yeast
11 S. cerevisiae. Vector DNAs of pKJ2 and pSW6 of
12 Preparation 2 were prepared. Both DNAs were treated
13 with restriction enzymes BglII and BamHI and the
14 ca. 1420 bp DNA fragment from pKJ2 and the ca. 7460
15 bp vector DNA fragment from pSW6 were gel purified and
16 ligated together. The recombinant ligation products
17 were transformed into competent cells of E. coli
18 strain DH5 (supE44, hsdR17, recA1, endA1, gyrA96,
19 thi-1, relA1), but any other good transforming strain
20 could be used, for example JM109 of Example 1.
21 Ampicillin (100 µg/ml) resistant transformants were
22 analysed by preparation of plasmid DNA, restriction
23 endonuclease digestion with BamHI and HindIII and
24 agarose gel electrophoresis. A clone with the
25 correct electrophoretic pattern pSMD1/111 was used for
26 the expression of streptokinase from its own signal
27 peptide sequence from the yeast S. cerevisiae.
28 Plasmid expression vector pSMD1/111 was transferred
29 into yeast (S. cerevisiae) strain BJ2168 according to
30 the method of Preparation 3.

31

32

33

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1 B) Secretion of Streptokinase using the pre-pro-
2 α-Factor Secretion Leader
3

4 A gene fusion to enable the streptokinase gene of
5 Preparation 4 to be expressed in yeast and to be
6 secreted by the yeast mating type α-factor
7 pre-pro-peptide was designed and constructed using
8 site-directed mutagenesis and molecular cloning see
9 SEQ ID NO:24. The construction involved mutagenesis to
10 create an α-factor-streptokinase fusion gene and
11 molecular cloning to reconstruct the DNA sequences
12 encoding the mature streptokinase protein sequence.
13 Single stranded DNA of pGC600 prepared from
14 E. coli strain RZ1032 (Example 1) was used as a
15 mutagenesis template with the 36-mer
16 oligonucleotide B B 3 6 2 4
17 (5'-GTCCAAGCTAACGCTTGGATAAAAGAATTGCTGGACC-3') SEQ ID
18 NO:25. Single stranded DNA from putative mutant
19 plaques were analysed by dideoxy sequence analysis
20 using the M13 universal sequencing primer (SEQ ID
21 NO:10) and a mutant clone, pGC614, with the desired
22 sequence was identified. In pGC614 the
23 OmpA-IGFII-Streptokinase signal peptide encoding
24 sequences of pGC600 have been deleted and the
25 α-factor linker encoding the C-terminal 5 amino acids
26 of the α-factor pro-peptide described in Preparation 2
27 have been inserted. To reconstruct the streptokinase
28 gene in a yeast expression vector, two stages of
29 genetic manipulation were required. First the
30 C-terminal portion of streptokinase was cloned into a
31 yeast expression vector and this new construct was used
32 to clone in the N-terminal α-factor-streptokinase
33 fusion portion of the gene, thus reconstructing a

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1 mature streptokinase coding region fused to the
2 α -factor pre-propeptide gene. Vector DNAs of pKJ2
3 and pSW6 (Preparation 2) were prepared and digested
4 with HindIII and BamHI and the ca. 485 bp. DNA
5 fragment from pKJ2 and the ca. 7750 bp. vector DNA
6 fragment from pSW6 were gel purified and ligated.
7 Recombinant ligation products were transformed into
8 competent cells of E. coli strain DH5. Ampicillin
9 resistant transformants were screened by preparation
10 of plasmid DNA, restriction endonuclease digestion with
11 HindIII and BamHI and agarose gel electrophoresis. A
12 clone with the correct electrophoretic pattern
13 pSMD1/119 was isolated. It contains DNA encoding
14 the C-terminal portion of streptokinase cloned into a
15 yeast expression vector. The DNA encoding the
16 N-terminal portion of streptokinase and the alpha-
17 factor adaptor sequence were next cloned into
18 pSMD1/119. Replicative form DNA of pGC614 was
19 prepared and treated with HindIII and ligated to
20 pSMD1/119 vector DNA which had been treated with
21 HindIII and phosphatased. The recombinant ligation
22 products were transformed into competent cells of
23 E. coli strain DH5. Ampicillin (100 μ g/ml) resistant
24 transformants were screened by preparation of plasmid
25 DNA, restriction endonuclease analysis with DraI and
26 agarose gel electrophoresis. A clone with the
27 correct electrophoretic pattern pSMD1/152 gave DraI
28 digestion products of ca. 4750, 1940, 1520 and 700 bp.
29 in length. pSMD1/152 was used for the expression and
30 secretion of streptokinase using the alpha factor
31 pre-pro-sequence from the yeast S. cerevisiae. Plasmid
32 expression vector pSMD1/152 was transferred into
33 yeast (S. cerevisiae) strain BJ2168 according to the
34 method of Preparation 3.

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1 EXAMPLE 5 - Construction of a Gene Encoding a Core
2 Streptokinase Protein

3

4 A gene encoding a truncated methionyl streptokinase
5 molecule (aa 16-383) was designed and constructed by
6 oligonucleotide directed loopout deletions and
7 molecular cloning; see SEQ ID NO:26. DNA encoding the
8 amino acids 2 to 21 of the OmpAL signal sequence, the
9 DNA encoding IGF-II, the DNA encoding the streptokinase
10 signal peptide and the first 15 amino acids of the
11 mature streptokinase protein in pGC600 of Example
12 4B were deleted by loopout mutagenesis using a
13 33-mer oligonucleotide BB3862:

14 5'-GAAATACTTACATATGAGCCAATTAGTTGTTAG-3'; SEQ ID NO:27.
15 Single stranded DNA was prepared from E. coli RZ1032
16 cells infected with pGC600 and used as the template
17 for mutagenesis with primer BB3862. Single stranded
18 DNA was prepared from putative mutant plaques and a
19 clone pGC604 containing the desired deletion was
20 identified by dideoxy sequence analysis using the M13
21 universal sequencing primer (SEQ ID NO:10, Example 1).

22

23 Amino acids 384 to 414 were deleted from
24 streptokinase by loopout mutagenesis using a
25 28-mer oligonucleotide BB3904:

26 5'-CCCGGGGATCCTTAGGCTAAATGATAGC-3'; SEQ ID NO:28.
27 The template for the mutagenesis was single
28 stranded DNA of M13JK1 of Example 10 containing the
29 ca. 500 bp HindIII-BamHI DNA fragment encoding the 3'
30 end of the streptokinase gene from pUC19SK of
31 Preparation 4. Single stranded DNA from putative
32 mutant plaques was prepared and a clone pGC605
33 containing the desired deletion was identified by

1 dideoxy sequence analysis using the M13 universal
2 sequencing primer (SEQ ID NO:10, Example 1).
3
4 The intact core streptokinase molecule was
5 reconstructed from the two mutated halves by a two
6 step ligation incorporating the NdeI-HindIII DNA
7 fragment from pGC604 (containing the DNA encoding the
8 N-terminal portion of the core streptokinase molecule)
9 and the HindIII-BamHI DNA fragment from pGC605
10 (containing the DNA encoding the C-terminal portion of
11 the core streptokinase molecule) into the vector DNA
12 pLGC2 of Example 6 below. First the pGC604 DNA was
13 digested with NdeI and HindIII. A DNA fragment of ca.
14 710 bp. was gel purified. Vector DNA was prepared
15 from pLGC2 of Example 6 and treated with NdeI and
16 HindIII and phosphatased. The linear vector DNA was
17 gel purified and the two fragments were ligated
18 together. The recombinant ligation products were
19 transformed into competent cells of E. coli strain
20 HW1110. Ampicillin (100 µg/ml) resistant
21 transformants were screened for the required clone
22 by preparation of plasmid DNA, restriction
23 endonuclease analysis with NdeI and HindIII followed
24 by agarose gel electrophoresis of the digestion
25 products. One construct with the correct
26 electrophoretic pattern, pGC617, was identified.
27
28 To clone the DNA encoding the C-terminal portion, the
29 same vector DNA (pLGC2) was treated with HindIII and
30 BamHI and phosphatased. The pGC605 DNA was treated
31 with HindIII and BamHI and a ca. 402 bp DNA fragment
32 was gel purified and ligated into the HindIII and BamHI
33 treated pLGC2 vector DNA. The recombinant ligation

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1 products were transformed into competent cells of
2 E. coli strain HW1110. Ampicillin (100 µg/ml)
3 resistant transformants were screened for the required
4 clone by preparation of plasmid DNA, restriction
5 endonuclease analysis with BamHI and HindIII, and
6 agarose gel electrophoresis of the digestion products.
7 One construct with the correct electrophoretic pattern
8 pGC618 was identified. Finally, to reconstruct the
9 intact core streptokinase gene from the two halves,
10 pGC617 DNA was treated with HindIII and BamHI and the
11 ca. 402 bp HindIII-BamHI fragment from pGC618 ligated
12 to it. pGC618 DNA was digested with HindIII and BamHI
13 and a ca. 402 bp HindIII-BamHI DNA fragment was gel
14 purified. pGC617 vector DNA was also treated with
15 HindIII and BamHI and a ca. 402 bp HindIII-BamHI DNA
16 fragment from pGC618 was ligated into it. The
17 ligation products were transformed into competent cells
18 of E. coli strain HW1110. Ampicillin resistant
19 transformants were screened by preparation of plasmid
20 DNA restriction endonuclease analysis with BamHI and
21 HindIII and agarose gel electrophoresis. A correct
22 construct, pGC606, was identified.

23

24 EXAMPLE 6 - Construction of Expression vectors
25 containing a Thrombin Cleavable Streptokinase-
26 Streptokinase Fusion Gene

27

28 1) Construction of a Secretion Vector for the
29 Expression of a Thrombin Cleavable Streptokinase-
30 Streptokinase Fusion

31

32 A gene encoding an OmpAL streptokinase-streptokinase
33 fusion linked by a thrombin cleavable linker sequence

1 VELQGVVPRG, identical to that at the thrombin
2 cleavage site in Factor XIII, was designed and
3 constructed by site directed mutagenesis and
4 molecular cloning (SEQ ID NO:29). A ca. 1.3 Kb
5 EcoRI-BamHI DNA fragment containing a streptokinase
6 gene was gel purified after treatment of the pUC19SK
7 vector DNA of Preparation 4 with EcoRI and BamHI. A
8 second DNA fragment encoding a streptokinase gene was
9 gel purified after BglII and SalI digestion of the
10 pKJ1 vector DNA of Example 4. A trimolecular ligation
11 was carried out between these two fragments and
12 EcoRI and SalI treated pGC517 vector DNA described
13 in Example 4, section 1A. The recombinant ligation
14 products were transformed into competent cells of
15 E. coli strain HW1110 (lacIq). Ampicillin (100 µg/ml)
16 resistant transformants were screened by preparation
17 of plasmid DNA, restriction endonuclease analysis with
18 EcoRI and SalI and agarose gel electrophoresis. A
19 clone with the correct electrophoretic pattern (pSD93)
20 was identified. pSD93 contains two tandem copies of the
21 streptokinase gene separated by a sequence containing
22 the bacteriophage lambda gene CII ribosome binding
23 site, and encoding the OmpA signal peptide sequence,
24 the streptokinase signal peptide sequence and the 5'
25 part of the IGF-II sequence from pKJ1. To remove this
26 unwanted intervening sequence and to replace it with
27 the desired thrombin cleavable linker sequence a
28 part of pSD93 was transferred into an M13
29 mutagenesis vector for mutagenesis. Plasmid pSD93 DNA
30 was digested with HindIII and a ca. 1530 bp DNA
31 fragment gel purified and ligated to HindIII
32 treated and phosphatased replicative form M13mp18
33 DNA. The recombinant ligation products were

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1 transformed into competent cells of E. coli strain
2 JM103 (Example 1). There are two possible fragment
3 orientations in such a construction. The
4 orientation of the clones was determined by preparation
5 of replicative form DNA and analysing the DNA fragments
6 produced after XmnI digestion and agarose gel
7 electrophoresis. One of the clones pSD95 which
8 contained the fragment in an inverted orientation
9 (thus preventing translation readthrough by virtue of
10 fusion to the α -fragment of β -galactosidase expressed
11 from the M13 mutagenesis vector) was used for
12 mutagenesis. Single stranded DNA template was
13 prepared from pSD95 and used for site directed
14 mutagenesis. The primer used was a 63-mer
15 oligonucleotide BB2938:
16 (5'-GATAACCCTAACGACAAAGTAGAGCTGCAGGGAGTAGTTCCCGTGGAAAT-
17 TGCTGGACCTGAG-3') (SEQ ID NO:30) designed to loop out
18 the gene cII ribosome binding site, the OmpAL IGF-II
19 sequence, the streptokinase signal peptide sequence in
20 pSD95 and to insert a DNA sequence encoding a thrombin
21 cleavable amino acid sequence. Single stranded DNAs
22 were prepared from putative mutant plaques and a
23 correct mutant pGC607 was identified using dideoxy
24 sequence analysis with primer BB2753 (SEQ ID NO:20) of
25 Example 4. Replicative form DNA of pGC607 was
26 prepared and was digested with HindIII and the
27 ca. 1277 bp HindIII DNA fragment gel purified and
28 ligated to HindIII treated and phosphatased pLGC1
29 vector DNA of Example 4. The recombinant ligation
30 products were transformed into competent cells of
31 E. coli strain HW1110. Ampicillin resistant
32 transformants were screened by preparation of plasmid
33 DNA, restriction endonuclease analysis using HindIII

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1 and agarose gel electrophoresis. This cloning
2 rebuilds the gene encoding a thrombin cleavable
3 streptokinase-streptokinase fusion in an expression
4 vector. A clone (pLGC2) carrying the insert in the
5 sense orientation was identified by dideoxy sequence
6 analysis using primers BB2754 (5'-GCTATCGGTGACACCAT-3')
7 SEQ ID NO:31 and BB3639 (5'-GCTGCAGGGAGTAGTTC-3') SEQ
8 ID NO:32. pLGC2 was used for the expression of
9 thrombin cleavable streptokinase-streptokinase fusion
10 protein in E. coli HW1110.

11
12 2) Construction of a Vector for the Intracellular
13 Expression of a Thrombin Cleavable Streptokinase-
14 Streptokinase Fusion Gene.
15

16 A thrombin cleavable methionyl-streptokinase-
17 streptokinase gene was designed and constructed by
18 molecular cloning. The gene was constructed from
19 the methionyl-streptokinase gene of Example 4 and the
20 HindIII DNA fragment from pGC607 of Example 6,
21 encoding the C-terminal portion of a first
22 streptokinase molecule, a thrombin cleavable linker and
23 an N-terminal portion of a second streptokinase
24 molecule.
25

26 Replicative form DNA of pGC607 was prepared and was
27 digested with HindIII and the ca. 1277 bp HindIII DNA
28 fragment was gel purified and ligated to HindIII
29 treated and phosphatased pGC603 vector DNA of
30 Example 4. The recombinant ligation products were
31 transformed into competent cells of E. coli strain
32 HW1110 (lacIq). Ampicillin (100 µg/ml) resistant
33 transformants were screened by preparation of plasmid

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1 DNA, restriction endonuclease analysis with HindIII,
2 BamHI and PstI and agarose gel electrophoresis of the
3 digestion products. One construct with the correct
4 electrophoretic pattern pLGC3, was used for the
5 intracellular expression of a thrombin cleavable
6 methionyl-streptokinase-streptokinase fusion protein.

7

8 EXAMPLE 7 - Construction of a Thrombin Cleavable Core
9 Streptokinase-core Streptokinase Fusion Gene

10

11 A gene encoding a core methionyl-streptokinase-core
12 streptokinase fusion linked by a thrombin
13 cleavable linker sequence VELQGVVPRG, identical to
14 that at the thrombin cleavage site in Factor XIII, was
15 designed and constructed by site directed
16 mutagenesis and molecular cloning see SEQ ID NO:33.
17 The core streptokinase-core streptokinase fusion gene
18 was constructed from the core streptokinase monomer
19 gene of Example 5 and a HindIII DNA fragment
20 containing the C-terminal portion of a core
21 streptokinase gene, a thrombin-cleavable linker and an
22 N-terminal portion of a core streptokinase gene. To
23 construct the HindIII DNA fragment containing the
24 appropriate deletions and encoding a thrombin-cleavable
25 linker, pGC607 of Example 6 was used as a template
26 for oligonucleotide directed mutagenesis. A 61-mer
27 oligonucleotide BB3861:

28 (5'-GCTATCATTAGCCGTAGAGCTGCAGGGAGTAGTTCCCTCGTGGAAAGCCAA-
29 TTAGTTGTTAG-3') SEQ ID NO:34 was used to delete the
30 streptokinase amino acids 384 to 414, to reconstruct
31 the thrombin cleavable linker sequence VELQGVVPRG and
32 to delete the first 15 amino acids of the N-terminus of
33 streptokinase. Single stranded DNA from putative

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1 mutant plaques was prepared and a correct clone,
2 pGC608, was identified by dideoxy sequence analysis
3 using sequencing primer BB2753 of example 8.
4 Replicative form DNA was prepared from pGC608 and used
5 in further construction.

6

7 To construct an intact core methionyl-streptokinase-
8 core-streptokinase fusion, pGC608 DNA was treated
9 with HindIII and the ca. 1140 bp HindIII DNA
10 fragment encoding the C-terminal portion of the core
11 streptokinase molecule, the thrombin cleavable linker
12 sequence and the N-terminal portion of a core
13 streptokinase molecule, was gel purified and ligated
14 to the vector DNA of pGC606 of Example 5 after
15 treatment with HindIII and phosphatase.. The
16 recombinant ligation products were transformed into
17 competent cells of E. coli strain HW1110 (lacIq).
18 Ampicillin (100 µg/ml) resistant transformants were
19 analysed by zymography as described in Example 11
20 below. A correct clone pLGC4, was identified.

21

22 EXAMPLE 8 - Construction of a Factor Xa-Cleavable
23 Hirudin-IEGR-Streptokinase Fusion Gene

24

25 A hirudin-streptokinase fusion has been designed
26 in which a full length hirudin molecule is joined to
27 full length streptokinase via an IEGR linker sequence
28 cleavable by factor Xa; see SEQ ID NO:35. The gene
29 encoding the hirudin-streptokinase protein was
30 constructed by site directed mutagenesis and molecular
31 cloning. In order to juxtapose the hirudin and
32 streptokinase genes, the DNA fragments encoding
33 these genes were ligated together. The streptokinase

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1 gene from plasmid pKJ2 of Example 4 was isolated by
2 gel purification of a ca. 1.4 kbp DNA fragment after
3 digestion of pKJ2 vector DNA with BglII and BamHI.
4 This DNA fragment contains all of the streptokinase
5 gene together with the DNA encoding the streptokinase
6 signal peptide sequence. This DNA fragment was then
7 ligated to BamHI treated pJK1 DNA of Preparation 2
8 which contains the hirudin encoding DNA sequence.
9 The recombinant ligation products were transformed
10 into competent cells of E. coli strain HW1110 (lacIq).
11 Ampicillin (100 µg/ml) resistant transformants were
12 screened by preparation of plasmid DNA, restriction
13 endonuclease digestion with HindIII and agarose gel
14 electrophoresis. There are two possible orientations
15 for the insert in this cloning event and correct
16 clones were identified as those which released a
17 ca. 1080 bp DNA fragment after HindIII digestion as
18 analysed on agarose gels. One such clone pJK3, which
19 contains the hirudin gene separated from the
20 streptokinase gene by the streptokinase signal
21 peptide sequence, was used in subsequent
22 manipulations. To create a template for mutagenesis
23 to delete the intervening sequences and to insert the
24 DNA encoding the factor Xa cleavable linker sequence,
25 the hirudin-streptokinase portion of pJK3 was
26 transferred to a mutagenesis vector M13mp18. Plasmid
27 DNA of pJK3 was digested with KpnI and BamHI and
28 the ca. 1490 bp DNA fragment gel purified and ligated
29 to KpnI and BamHI treated M13mp18 replicative form
30 DNA. The recombinant ligation products were
31 transfected into competent cells of E. coli JM103
32 (Example 1). Single stranded DNA was prepared from
33 putative recombinant plaques and a correct clone

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1 pSMD1/100 (1.1) was identified. To delete the
2 streptokinase signal peptide sequence and to insert the
3 DNA encoding the factor Xa linker sequence single
4 stranded DNA of pSMD1/100 (1.1) was used as a template
5 for mutagenesis with a 46-mer oligonucleotide BB3317:
6 (5'-CACTCAGGTCCAGCAATTCTACCTTCGATCTGCAGATATTCTTCTG-3')
7 SEQ ID NO:36. Single stranded DNA from putative mutant
8 plaques were prepared and a mutant pGC615 was
9 identified by DNA sequence analysis using the
10 sequencing primer BB3510 (5'-CACTATCAGTAGCAAAT-3') SEQ
11 ID NO:37. pGC615 contains the C-terminal portion
12 of the hirudin gene linked to the mature streptokinase
13 protein coding sequence. In order to reconstruct the
14 hirudin gene, replicative form DNA of pGC615 was
15 treated with KpnI and BamHI, the ca. 1320 bp DNA
16 fragment gel purified and ligated to KpnI and BamHI
17 treated pJC80 of Preparation 2. The recombinant
18 ligation products were transformed into competent cells
19 of E. coli strain DH5 (Example 4). Ampicillin
20 (100 µg/ml) resistant transformants were screened by
21 preparation of plasmid DNA, restriction endonuclease
22 analysis with KpnI, BamHI and HindIII and agarose gel
23 electrophoresis. A clone with the correct
24 electrophoretic pattern pSMD1/139 was identified.
25 This plasmid contains DNA encoding the complete
26 factor Xa cleavable hirudin-streptokinase fusion
27 molecule.

28

29 EXAMPLE 9 - Construction of a Vector for the Expression
30 of a Factor Xa Cleavable Hirudin-IEGR-Streptokinase
31 Fusion Molecule

32

33 To construct a vector for the expression of the

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1 hirudin-IEGR-streptokinase gene, DNA of pSMD1/139 of
2 Example 8 was treated with HindIII and a ca. 963 bp
3 DNA fragment encoding part of the yeast alpha factor
4 secretion signal, all of hirudin, the factor Xa linker
5 and the 5' part of streptokinase as far as the internal
6 HindIII site in the streptokinase sequence was gel
7 purified. This fragment was then ligated to HindIII
8 treated and phosphatased DNA of pSMD1/119 of Example
9 4. The recombinant ligation products were transformed
10 into competent cells of E. coli strain DH5
11 (Example 4). Ampicillin resistant transformants were
12 screened by preparation of plasmid DNA, restriction
13 endonuclease digestion with KpnI and BamHI and
14 agarose gel electrophoresis. It is possible to
15 obtain two orientations of the HindIII insert and one
16 clone in the correct orientation pSMD1/146 was
17 identified as releasing a ca. 1311 bp fragment after
18 KpnI and BamHI treatment. pSMD1/146 contains the full
19 length fusion gene under the control of the
20 regulatable PAL promoter described in Preparation 2,
21 and has been designed for the regulated expression
22 and secretion of the factor Xa-cleavable
23 hirudin-streptokinase fusion protein. pSMD1/146
24 plasmid DNA was prepared and used to transform yeast
25 strain BJ2168 (Preparation 3) according to the method
26 of Sherman, F. et al., (Methods in Yeast Genetics, Cold
27 Spring Harbor Laboratory (1986)).
28
29
30
31
32
33

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1 EXAMPLE 10 - Construction of a Factor Xa Cleavable
2 Streptokinase-IEGR-Hirudin Fusion Gene and its
3 Expression Vector

4

5 A gene encoding a streptokinase-hirudin fusion
6 protein linked via a Factor Xa cleavage site (IEGR)
7 was constructed by site-directed mutagenesis and
8 molecular cloning SEQ ID NO:38. In order to juxtapose
9 the streptokinase and hirudin genes, DNA fragments
10 encoding these two gene were ligated together. The
11 pUC19SK vector DNA of Preparation 4 was prepared and
12 treated with HindIII and BamHI and the ca. 500 bp DNA
13 fragment containing the 3' end of the streptokinase
14 gene was gel purified. This fragment was ligated to
15 M13mp19 replicative form DNA treated with HindIII and
16 BamHI. The recombinant ligation mixture was
17 transfected into competent cells of E. coli strain
18 JM103 (Example 1). Single stranded DNA was prepared
19 from putative recombinant plaques and the required
20 clone M13JK1 identified by dideoxy sequence analysis
21 using the M13 universal sequencing primer (SEQ ID
22 NO:10, Example 1). M13JK1 contains the C-terminal
23 portion of the streptokinase gene. The α -factor
24 hirudin gene was then cloned into M13JK1 to
25 juxtapose both sequences. Plasmid DNA of pJK1 of
26 Preparation 2 was digested with BglII and BamHI and
27 a ca. 465bp DNA fragment encoding the α -factor hirudin
28 fusion was gel purified. This DNA fragment was then
29 ligated to BamHI treated replicative form DNA of
30 M13JK1. The recombinant ligation products were
31 transfected into competent cells of E. coli strain
32 JM103. Single stranded DNA from putative recombinant
33 plaques were prepared and a correct clone

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1 SMD1/100.3 identified by dideoxy sequence analysis
2 using M13 universal sequencing primer (SEQ ID NO:10,
3 Example 1. SMD1/100.3 contains the C-terminal portion
4 of the streptokinase gene and the complete hirudin
5 gene separated by the α -factor encoding sequence
6 described in Preparation 2. In order to delete this
7 sequence and replace it with a factor Xa-cleavable
8 linker sequence, SMD1/100.3 was used as a template
9 for site-directed mutagenesis. Single stranded DNA
10 of SMD1/100.3 was prepared and used for mutagenesis
11 using a 47-mer mutagenesis primer BB3318:
12 (5'-TCGGTGTAAACAACTCTTCTACCTTCGATTTCGTTAGGGTTATC-3')
13 (SEQ ID NO:40). Single stranded DNA from putative
14 mutant plaques were prepared and the required mutation
15 pGC616 identified by dideoxy sequence analysis
16 using the sequencing primer BB2018:
17 (5'-GC GGCTTGGGGTACCTCACCA GTGACACATTGG-3') (SEQ ID
18 NO:2). pGC616 contains an additional mutation
19 inadvertently introduced by the mutagenesis procedure.
20 This was corrected by a further mutagenic step. Single
21 stranded DNA of pGC616 was prepared and used as a
22 template for mutagenesis with a 21-mer
23 oligonucleotide BB3623 (5'-GTGTAAACAACTCTACCTTCG-3')
24 (SEQ ID NO:40). Single stranded DNA from putative
25 mutant plaques was prepared and a correct clone pGC620
26 identified by dideoxy sequence analysis with the
27 sequencing primer BB2018 (SEQ ID NO:2). pGC620
28 contains the C-terminal portion of the streptokinase
29 gene and the complete hirudin gene fused via DNA
30 encoding a factor Xa-cleavable linker. The intact
31 factor Xa-cleavable streptokinase-hirudin fusion gene
32 was reconstructed in two steps. The C-terminal
33 streptokinase-hirudin sequence from pGC620 was cloned

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1 into the yeast expression vector pSW6 of
2 Preparation 2 and then the N-terminal portion of
3 streptokinase was cloned into the new vector to
4 create the full length streptokinase-hirudin fusion
5 gene.

6

7 Replicative form DNA of pGC620 was treated with HindIII
8 and BamHI and a ca. 710 bp HindIII-BamHI DNA
9 fragment encoding the 3' end of streptokinase, the
10 intervening factor Xa-cleavable linker DNA sequence and
11 all of the hirudin gene was gel purified. This
12 ca. 710 bp DNA fragment was ligated to pSW6 of
13 Preparation 2 digested with HindIII and BamHI. The
14 recombinant ligation products were transformed into
15 competent cells of E. coli strain DH5 (Example 4).
16 Ampicillin (100 µg/ml) resistant transformants were
17 screened by preparation of plasmid DNA, restriction
18 endonuclease analysis using HindIII and BamHI
19 and agarose gel electrophoresis. A clone with the
20 correct electrophoretic pattern pSMD1/143 was
21 identified. The intact fusion gene was then
22 constructed by cloning the N-terminal portion of
23 α-factor-streptokinase into pSMD1/143. Replicative
24 form DNA of pGC614 of Example 4 was treated with
25 HindIII and the ca. 750 bp DNA fragment containing the
26 N-terminal portion of α-factor-streptokinase gel
27 purified and ligated to HindIII treated and
28 phosphatased pSMD1/143 vector DNA. The recombinant
29 ligation products were transformed into competent cells
30 of E. coli strain DH5. Ampicillin (100 µg/ml)
31 resistant transformants were screened by preparation of
32 plasmid DNA, restriction endonuclease digestion with
33 DraI and agarose gel electrophoresis. A clone in the

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1 correct orientation pSMD1/159 was identified as giving
2 rise to 4 fragments of sizes of about 4750 bp,
3 2140 bp, 1526 bp, and 692 bp after DraI digestion.
4 pSMD1/159 was used for the expression of the factor
5 Xa-cleavable streptokinase-hirudin fusion protein.
6 pSMD1/159 plasmid DNA was prepared and used to
7 transform yeast strain BJ2168 (Preparation 5) according
8 to the method of Sherman, F. et al., (Methods in
9 Yeast Genetics, Cold Spring Harbour Laboratory (1986)).
10

11 EXAMPLE 11 - Expression of Monomer Streptokinase
12 Constructs

13
14 Expression

15
16 Competent cells of E. coli strain JM103 (Example 1)
17 were transformed with DNA of the streptokinase
18 expression vectors of Examples 4, 5, 6 and 7. The
19 lacIq gene in the expression host is desirable to
20 repress transcription from the tac promoter used in all
21 of the E. coli expression constructs. All media for
22 the growth of recombinant E. coli strains were as
23 described in Maniatis et al. Using 1 litre shake
24 flasks, cultures of recombinant E. coli containing
25 streptokinase expression vectors were grown in 250 ml
26 batches of 2TY medium containing 100 µg/ml of
27 carbenicillin at 37°C in an orbital shaker. The
28 optical density of the cultures were monitored at
29 600 nm. When the culture reached an OD 600 nm of 0.5,
30 expression from the tac promoter was induced by
31 the addition of isopropyl-β-D-thiogalactoside (IPTG) to
32 a final concentration of 1 mM. After growth for 30 to
33 240 min the cells were harvested by centrifugation.

1 SDS-PAGE Separation

2

3 The ability of the recombinant E. coli cells to express
4 streptokinase was assayed using zymography. The
5 quantity and molecular weight of streptokinase
6 activity of an E. coli culture was estimated by the
7 following protocol. A 1 ml aliquot of the culture
8 was removed, the cells were harvested by
9 centrifugation (14 000xg) for 5 mins and resuspended
10 in 200 µl of loading buffer (125 mM Tris.HCl pH 6.8,
11 10% glycerol (w/v), 0.01% (w/v) bromophenol
12 blue, 1% (v/v) 2-mercaptoethanol, 6M urea). An
13 aliquot of this mixture was applied to an SDS-PAGE gel
14 and the protein separated by electrophoresis. The
15 quantity of protein loaded onto the gel was varied
16 by altering the size of the aliquot according to the
17 optical density of the culture upon harvesting.
18 Generally, 10 µl of the mixture from a culture of OD
19 600 nm of 1.0 was used for each lane.

20

21 Zymography

22

23 After electrophoresis the polyacrylamide gel was washed
24 in 2% (w/v) Triton X-100 (3x20 mins) followed by
25 water washes (3x20 mins) to remove the SDS and allow
26 renaturation of the streptokinase molecule.

27

28 The washed SDS-PAGE gel was then overlayed with an
29 agarose mixture prepared as follows. 200 mg of agarose
30 was dissolved in 18 ml distilled and deionised water
31 (dH₂O) and allowed to cool to 55-60°C. To this 200 mg
32 of MARVEL (trade mark of Premier Brands, U.K. Ltd. P.O.
33 Box 171, Birmingham, B30 2NA, U.K.) (casein) dissolved

1 in 2 ml of dH₂O, 1 ml of 1M Tris.HCl pH 8.0 and 600
2 μl of 5M NaCl were added. Just before pouring over
3 the washed SDS-PAGE gel, 700 μl of plasminogen at
4 300 μg/ml (Sigma P-7397 10 mg/ml in 50 mM Tris.HCl pH
5 7.5) was added and mixed thoroughly. The mixture was
6 poured over the gel and once set was incubated at
7 37°C for 2 hours when it could be inspected.
8 Plasminogen activator activity (streptokinase
9 activity) was detected by plasmin digestion of
10 the opaque casein containing overlay which produced
11 clear zones. The position of the zones on the gel
12 was directly related to the size of the active
13 molecules.

14
15 The recombinant *E. coli* JM103 strains containing
16 monomer streptokinase expression vectors pKJ2 of
17 Example 4 and pLGC1 of Example 4 both expressed
18 streptokinase activity with a molecular weight
19 of approximately 47 kDa (Figure 5).

20
21 EXAMPLE 12 - Expression of a Thrombin Cleavable
22 Streptokinase-Streptokinase Fusion Protein.

23
24 A recombinant *E. coli* HW1110 (*lacIq*) strain (Example
25 1) containing pLGC2 of Example 6, the thrombin
26 cleavable streptokinase- streptokinase fusion gene,
27 was expressed and analysed according to the
28 expression and zymography protocols of Example 11.
29 The *E. coli* JM103/pLGC2 strain expressed streptokinase
30 activities of several molecular weights, predominantly
31 of 110 kDa and 47 kDa (Figure 5). Cleavage analysis is
32 described in Example 13 below.

33

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1 EXAMPLE 13 - Cleavage of the Thrombin Cleavable
2 Streptokinase-streptokinase Fusion Protein by Thrombin

3
4 Using 1 litre shake flasks, a 3 litre culture
5 of E. coli JM103 (Example 1) containing pLGC2 of
6 Example 6 was grown in 500 ml batches in 2TY medium
7 containing 100 mcg/ml carbenicillin at 37°C with
8 vigorous shaking in an orbital shaker. When the
9 optical density of the cultures reached an O.D.
10 600 nm of 0.5 the expression of the streptokinase-
11 streptokinase fusion protein was induced by the
12 addition of IPTG to a final concentration of 1 mM. The
13 cultures were incubated at 37°C with vigorous shaking
14 for a further 4 hours when they were harvested by
15 centrifugation at 8,000 r.p.m. for 10 mins. The cells
16 were resuspended in 10 ml of ice cold TS buffer
17 (10 mM Tris.HCl pH 7.5, 20% (w/v) sucrose). 348 µl
18 of 0.5 M EDTA was added and the mixture incubated on
19 ice for 10 mins. The cells were harvested by
20 centrifugation at 8,000 r.p.m. for 5 min at 4°C and
21 the supernatant discarded. The cells were resuspended
22 in 6.25 ml of ice cold sterile H₂O and incubated on
23 ice for 10 min. The cells were harvested by
24 centrifugation at 8,000 rpm. for 5 min at 15,000 g for
25 30 min at 4°C and the supernatant discarded. The cells
26 were resuspended in 48 ml of ARG buffer (20 mM Tris.HCl
27 pH 7.5, 10 mM MgCl₂, 10mM 2-b-mercaptoethanol, 0.5 mM
28 phenylmethyl sulphonyl fluoride, 12 mM N-tosyl-L-phenylalanine chloromethyl ketone) and
29 sonicated on ice (6 x 30 sec. bursts on maximum power,
30 MSE SONIPREP 150 (trade mark)). The cell sonicate was
31 centrifuged at 15,000 g for 30 min at 4°C. The
32 supernatant was decanted and assayed for streptokinase
33

1 activity using the S2251 (KabiVitrum Ltd, KabiVitrum
2 House, Riverside Way, Uxbridge, Middlesex, UB8 2YF, UK)
3 chromogenic assay for the streptokinase activation of
4 plasminogen. S2251 is a specific tripeptide
5 chromogenic substrate for plasmin. 25 μ l of 0.1 M
6 Tris.HCl pH 8.0 was placed in wells 2 to 12 of 96
7 well plates. Aliquots of the sample (25 μ l) were
8 placed in wells 1 and 2, and two-fold dilutions made by
9 mixing and pipetting from wells 2 to 3, 3 to 4 and so
10 on to well 11. A 100 μ l aliquot of a
11 plasminogen/S2251 mixture (40 μ l plasminogen 300 μ g/ml,
12 220 μ l S2251 1 mg/ml, 1.04 ml 0.1 M Tris.HCl pH
13 7.5) was added to each well and the plate incubated
14 at 37°C for 30 min. The reaction was terminated by
15 the addition of 50 μ l of 0.5 M acetic acid. The
16 absorbance was read at 405 nm using an automatic plate
17 reader. Quantification was performed by comparison
18 with a standard streptokinase preparation. The
19 analysis showed that the supernatant contained
20 approximately 2560 u/ml of streptokinase activity.
21
22 Solid ammonium sulphate was slowly added to the
23 supernatant to 15% saturation (4.03 g) and allowed to
24 dissolve for 15 min at room temperature. The mixture
25 was then centrifuged for 30 min at 15,000 g at room
26 temperature. The supernatant was decanted and
27 additional solid ammonium sulphate was added to 40%
28 saturation (7.27 g), and allowed to dissolve. The
29 mixture was centrifuged for 30 min at 15,000 g at room
30 temperature and the supernatant discarded. The
31 pelleted protein (the 15-40% cut), was resuspended in
32 10 ml of ARG buffer. A portion of the 15-40% cut was
33 assayed using the S2251 chromogenic assay and was found
34 to contain 18,432 u/ml of streptokinase activity.

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1 The ability of thrombin to cleave the streptokinase-
2 streptokinase fusion protein at the thrombin cleavable
3 linker was assessed by an in vitro cleavage assay and
4 zymography. A 5 μ l aliquot of the 15-40% cut was
5 mixed with 45 μ l of ARG buffer to dilute the
6 protein ten-fold. 10 μ l of this mixture was
7 incubated with 5 u/ml of thrombin in a final volume
8 of 50 μ l at 37°C for 14 hours. Aliquots (10 μ l) of
9 the thrombin cleavage reactions were analysed by
10 zymography according to the method of Example 11. The
11 results are shown in Figure 6. The streptokinase-streptokinase fusion protein (Mr 110
12 kDa), was quantitatively cleaved whilst the lower
13 molecular weight streptokinase activity (Mr 47 kDa) was
14 not cleaved by thrombin. Thus the streptokinase-
15 streptokinase fusion protein is cleavable by
16 thrombin.
17

18

19 EXAMPLE 14 - Expression of a Factor Xa Cleavable
20 Streptokinase-IEGR-hirudin Fusion Gene
21

22 Plasmid expression vector pSMD1/159 of Example 10 was
23 transferred into yeast (S. cerevisiae) strain BJ2168
24 according to the method of Preparation 3. Using
25 500 ml shake flasks, cultures of yeast containing
26 pSMD1/159 were grown in 100 ml batches of 0.67%
27 synthetic complete medium yeast nitrogen base, with
28 amino acids minus leucine and 1% glucose as a carbon
29 source. After overnight growth at 30°C, the cells
30 were harvested by centrifugation at 3,000 rpm for
31 10 min and resuspended in the same synthetic complete
32 medium except having 1% galactose and 0.2% glucose as
33 the carbon source and the addition of sodium phosphate

1 (to 50 mM) pH 7.2. This induces the expression of
2 the streptokinase-hirudin fusion gene from the hybrid
3 PGK promoter. Cells were grown in the induction
4 medium for 3 days. After this period, the supernatant
5 was harvested by centrifugation. The broth was
6 assayed for both streptokinase activity according to
7 the S2251 assay procedure of Example 13 and hirudin
8 activity according to the thrombin inhibition assay
9 of Example 2. Both activities were detected and
10 secreted to the medium.

11

12 EXAMPLE 15 - Expression of a Factor Xa Cleavable
13 Hirudin-IEGR-Streptokinase Fusion Gene

14

15 Plasmid expression vector pSMD1/146 of Example 9
16 was transferred into yeast (S. cerevisiae) strain
17 BJ2168 according to the method of Preparation 3. The
18 culture was incubated, expressed, harvested and the
19 hirudin and streptokinase activities assayed according
20 to the methods of Examples 2 and 13. Both
21 streptokinase and hirudin activities were detected and
22 secreted to the medium.

23

24

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SEQUENCE LISTINGS

SEQ. ID NO: 1

SEQUENCE TYPE: nucleotide with corresponding protein
 SEQUENCE LENGTH: 201 base pairs
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: synthetic DNA
 SOURCE: synthetic
 FEATURES: hirudin type HV-1 gene
 from 195 to 201 bp non-translated stop codons
 SEQUENCE:

GTT	GTT	TAC	ACC	GAC	TGT	ACT	GAA	TCC	GGA	CAA	AAC	CTG	TGT	TTG	45
CAA	CAA	ATG	TGG	CTG	ACA	TGA	CTT	AGG	CCT	GTT	TTG	GAC	ACA	AAC	
Val	Val	Tyr	Thr	Asp	Cys	Thr	Glu	Ser	Gly	Gln	Asn	Leu	Cys	Leu	
															15
5															
TGT	GAG	GGT	TCT	AAC	GTC	TGT	GGT	CAG	GGT	AAC	AAA	TGC	ATC	CTG	90
ACA	CTC	CCA	AGA	TTG	CAG	ACA	CCA	GTC	CCA	TTG	TTT	ACG	TAG	GAC	
Cys	Glu	Gly	Ser	Asn	Val	Cys	Gly	Gln	Gly	Asn	Lys	Cys	Ile	Leu	
20															
25															
GGT	TCC	GAC	GGT	GAA	AAG	AAC	CAA	TGT	GTC	ACT	GGT	GAA	GGT	ACC	135
CCA	AGG	CTG	CCA	CTT	TTC	TTG	GTT	ACA	CAG	TGA	CCA	CTT	CCA	TGG	
Gly	Ser	Asp	Gly	Glu	Lys	Asn	Gln	Cys	Val	Thr	Gly	Glu	Gly	Thr	
35															
40															
CCA	AAG	CCG	CAG	TCC	CAC	AAC	GAT	GGA	GAT	TTC	GAA	GAA	ATC	CCA	180
GGT	TTC	GGC	GTC	AGG	GTG	TTG	CTA	CCT	CTA	AAG	CTT	CTT	TAG	GGT	
Pro	Lys	Pro	Gln	Ser	His	Asn	Asp	Gly	Asp	Phe	Glu	Glu	Ile	Pro	
50															
55															
60															
GAA	GAA	TAT	CTG	CAG	TAATAG										201
CTT	CTT	ATA	GAC	GTC	ATTATC										
Glu	Glu	Tyr	Leu	Gln											
65															

***** END OF SEQ ID NO: 1 *****

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SEQ. ID NO:2

SEQUENCE TYPE: nucleotide

SEQUENCE LENGTH: 223 base pairs

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA

SOURCE: synthetic

FEATURES: oligomers designed for construction of
synthetic type HV-1 gene.

SEQUENCE:

BB2011	BB2013	50
AGCTTACCTG CCATGGTTGT TTACACCGAC TGTACTGAAT C ATGGAC GGTACCAACA AATGTGGCTG ACATGACTTA GGCCTGTT TT	CGGACAAAAA 	
BB2012		
BB2014		
BB2015		
CCTGTGTTTG TGTGAGGGTT CTAACGTC TG TGGTCAGGGT AACAAATGCA GGACACAAAC ACACCTCCAA GATTGCAGACACC AG TCCA TTGTTTACGT	100	
BB2016	BB2017	150
TCCTGGGTTC CGACGGTG AA AAGAACCAAT GTGTCACTGG TGAAGGTACC AGGACCCAAG GCTGCCACTTTCT T GGTAA CACAGTGACC ACTTCCATGG	BB2018	
BB2019		
CCA AAGCCGC AGTCCCACAA CGATGGAGAT TTCGAAGAAA TC GGTTTCGGCG TCAGGGTGTT GCTACCTCTA AAGCTTCTTT AGGGTCTTC	191	
BB2020		
BB2021		
CCAGAAGAATATCTGCAG TAATAGGGAT CCG TTATAGACGTC ATTATCCCTA GGCTTAA	223	
BB2022		

***** END OF SEQ ID NO: 2 *****

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70

SEQ. ID NO:3

SEQUENCE TYPE: nucleotide

SEQUENCE LENGTH: 19 base pairs

FEATURES: Universal sequencing primer complementary
to the universal primer region of pUC19.

SEQUENCE:

CAGGGTTTTC CCAGTCACG

19

***** END OF SEQ ID NO: 3 *****

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SEQ ID NO: 4

SEQUENCE TYPE: nucleotide
 SEQUENCE LENGTH: 7859 base pairs
 STRANDEDNESS: single
 TOPOLOGY: circular
 SOURCE: experimental
 FEATURES: Sequence of plasmid pSW6
 SEQUENCE:

TTCCCATGTC	TCTACTGGTG	GTGGTGCTTC	TTTGGAAATT	TTGGAAGGTA	50
AGGAATTGCC	AGGTGTTGCT	TTCTTATCCG	AAAAGAAATA	AATTGAATTG	100
AATTGAAATC	GATAGATCAA	TTTTTTTCTT	TTCTCTTCC	CCATCCTTTA	150
CGCTAAAATA	ATAGTTTATT	TTATTTTTG	AATATTTTTT	ATTTATATAAC	200
GTATATATAG	ACTATTATTT	ACTTTAAATA	GATTATTAAG	ATTTTTTATTA	250
AAAAAAAATT	CGTCCTCTT	TTTAATGCCT	TTTATGCAGT	TTTTTTTCC	300
CATTGATAT	TTCTATGTT	GGGTTTCAGC	GTATTTAAG	TTTAATAACT	350
CGAAAATTCT	GCGTTTCGAA	AAAGCTCTGC	ATTAATGAAT	CGGCCAACGC	400
GCGGGGAGAG	GCGGTTTGC	TATTGGGCGC	TCTTCCGCTT	CCTCGCTCAC	450
TGACTCGCTG	CGCTCGGTG	TTCGGCTGCG	GCGAGCGGT	TCAGCTCACT	500
CAAAGGCGGT	AATACGGTTA	TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	550
AACATGTGAG	CAAAGGCCA	GCAAAAGGCC	AGGAACCGTA	AAAAGGCCGC	600
GTTGCTGGCG	TTTTCCATA	GGCTCCGCC	CCCTGACGAG	CATCACAAAA	650
ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	700
CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCCT	750
GCCGCTTACC	GGATACCTGT	CCGCCTTCT	CCCTTCGGGA	AGCGTGGCGC	800
TTTCTCATAG	CTCACGCTGT	AGGTATCTCA	GTTCGGTGT	GGTCGTTCGC	850
TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	GTTCAGCCCG	ACCGCTGC	900
CTTATCCGGT	AACTATCGTC	TTGAGTCCAA	CCCAGTAAGA	CACGACTTAT	950
CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	1000
GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	1050
AAGGACAGTA	TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	1100
AAAGAGTTGG	TAGCTCTTGA	TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	1150
GGTTTTTTG	TTTGAAGCA	GCAGATTACG	CGCAGAAAAA	AAGGATCTCA	1200
AGAAGATCCT	TTGATCTTT	CTACGGGGTC	TGACGCTCAG	TGGAACGAAA	1250
ACTCACGTTA	AGGGATTTG	GTCATGAGAT	TATCAAAAG	GATCTTCACC	1300
TAGATCCTTT	TAAATTAAAA	ATGAAGTTT	AAATCAATCT	AAAGTATATA	1350
TGAGTAAACT	TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	1400
TCTCAGCGAT	CTGTCTATT	CGTTCATCCA	TAGTTGCCTG	ACTCCCCGTC	1450
GTGTAGATAA	CTACGATACG	GGAGGGCTTA	CCATCTGGCC	CCAGTGTGTC	1500
AATGATAACG	CGAGACCCAC	GCTCACCGGC	TCCAGATTTA	TCAGCAATAA	1550
ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA	GTGGTCTG	AACTTTATCC	1600
GCCTCCATCC	AGTCTATTAA	TTGTTGCCGG	GAAGCTAGAG	TAAGTAGTTC	1650
GCCAGTTAAT	AGTTTGC	ACGTTGTTGC	CATTGCTACA	GGCATCGTGG	1700
TGTCACGCTC	GTCGTTGGT	ATGGCTTCAT	TCAGCTCCGG	TTCCCAACGA	1750
TCAAGGCGAG	TTACATGATC	CCCCATGTTG	TGCAAAAAG	CGGTTAGCTC	1800
CTTCGGTCCT	CCGATCGTTG	TCAGAAGTAA	GTTGGCCGCA	GTGTTATCAC	1850
TCATGGTTAT	GGCAGCACTG	CATAATTCTC	TTACTGTCAT	GCCATCCGTA	1900
AGATGCTTT	CTGTGACTGG	TGAGTACTCA	ACCAAGTCAT	TCTGAGAATA	1950

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GTGTATGCGG	CGACCGAGTT	GCTCTTGC	GGCGTCAACA	CGGGATAATA	2000
CCCGGCCACA	TAGCAGAACT	TTAAAAGTGC	TCATCATTGG	AAAACGTTCT	2050
TCGGGGCGAA	AACTCTCAAG	GATCTTACCG	CTGTTGAGAT	CCAGTTCGAT	2100
GTAACCCACT	CGTGACCCCA	ACTGATCTTC	AGCATCTTT	ACTTTCACCA	2150
GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	AAAATGCCGC	AAAAAAGGGA	2200
ATAAAGGGCGA	CACGGAATG	TTGAATACTC	ATACTCTTCC	TTTTTCAATA	2250
TTATTGAAGC	ATTATATCAGG	GTTATTGTCT	CATGAGCGGA	TACATATTTG	2300
AATGTATTAA	AAAAAAATAA	CAAATAGGGG	TTCCGCGCAC	ATTTCCCCGA	2350
AAAGTGCCAC	CTGACGTCTA	AGAAACCATT	ATTATCATGA	CATTAACCTA	2400
TAAAAAATAGG	CGTATCACGA	GGCCCTTTCG	TCTTCAAGAA	TTCTGAACCA	2450
GTCCTAAAAC	GAGTAAATAG	GACCGGCAAT	TCTTCAAGCA	ATAAACAGGA	2500
ATACCAATT	TTAAAAGATA	ACTTAGTCAG	ATCGTACAAT	AAAGCTAGCT	2550
TTGAAGAAAA	ATGCCCTTA	TTCAATCTT	GCTATAAAA	ATGGCCCAAA	2600
ATCTCACATT	GGAAAGACATT	TGATGACCTC	ATTTCTTCA	ATGAAGGGCC	2650
TAACGGAGTT	GACTAATGTT	GTGGGAAATT	GGAGCGATAA	GCGTGCTTCT	2700
GCCGTGGCCA	GGACAAACGTA	TACTCATCAG	ATAACAGCAA	TACCTGATCA	2750
CTACTTCGCA	CTAGTTCTC	GGTACTATGC	ATATGATCCA	ATATCAAAGG	2800
AAATGATAGC	ATTGAAGGGAT	GAGACTAAC	CAATTGAGGA	GTGGCAGCAT	2850
ATAGAACAGC	TAAAGGGTAG	TGCTGAAGGA	AGCATAACGAT	ACCCCGCATG	2900
GAATGGGATA	ATATCACAGG	AGGTACTAGA	CTACCTTCA	TCCTACATAA	2950
ATAGACGCAT	ATAAGTACGC	ATTTAAGCAT	AAACACGCAC	TATGCCGTTC	3000
TTCTCATGTA	TATATATATA	CAGGCAACAC	GCAGATATAG	GTGCGACGTG	3050
AACAGTGAGC	TGTATGTGCG	CAGCTCGCGT	TGCATTTTCG	GAAGCGCTCG	3100
TTTCGGAAA	CGCTTGAAG	TTCCTATTCC	GAAGTTCCTA	TTCTCTAGAA	3150
AGTATAGGAA	CTTCAGAGCG	CTTTTGAAA	CCAAAAGCGC	TCTGAAGACG	3200
CACTTCAAA	AAACCAAAA	CGCACCGGAC	TGTAACGAGC	TACTAAAATA	3250
TTGCGAATAC	CGCTTCCACA	AACATTGCTC	AAAAGTATCT	CTTTGCTATA	3300
TATCTCTGTG	CTATATCCCT	ATATAACCTA	CCCATCCACC	TTTCGCTCCT	3350
TGAACTTGCA	TCTAAACTCG	ACCTCTACAT	TTTTTATGTT	TATCTCTAGT	3400
ATTACTCTTT	AGACAAAAAA	ATTGTAGTAA	GAACTATTCA	TAGAGTGAAT	3450
CGAAAACAAT	ACGAAAATGT	AAACATTTC	TATACGTAGT	ATATAGAGAC	3500
AAAATAGAAG	AAACCGTTCA	TAATTTCCTG	ACCAATGAAG	AATCATCAAC	3550
GCTATCACTT	TCTGTCACA	AAGTATGC	AATCCACATC	GGTATAGAAT	3600
ATAATCGGGG	ATGCCCTTAT	CTTGAAAAAA	TGCACCCGCA	GCTTCGCTAG	3650
TAATCAGTAA	ACGGGGGAAG	TGGAGTCAGG	CTTTTTTAT	GGAAGAGAAA	3700
ATAGACACCA	AAGTAGCCTT	CTTCTAACCT	TAACGGACCT	ACAGTGCAAA	3750
AAGTTATCAA	GAGACTGCAT	TATAGAGCGC	ACAAAGGAGA	AAAAAAGTAA	3800
TCTAAGATGC	TTTGTAGAA	AAATAGCGCT	CTCGGGATGC	ATTTTTGTAG	3850
ACAAAAAAAG	AAGTATAGAT	TCTTGTGTTG	TAAAATAGCG	CTCTCGCGTT	3900
GCATTTCTGT	TCTGTAAAAA	TGCAGCTCAG	ATTCTTGTGTT	TGAAAAAATTA	3950
GCGCTCTCGC	GTTGCATT	TGTTTACAA	AAATGAAGCA	CAGATTCTC	4000
GTTGGTAAAA	TAGCGCTTTC	CGCGTGCATT	TCTGTTCTGT	AAAAATGCAG	4050
CTCAGATTCT	TTGTTGAAA	AATTAGCGCT	CTCGCGTTGC	ATTTTTGTTC	4100
TACAAAATGA	AGCACAGATG	CTTCGTTAAC	AAAGATATGC	TATTGAAGTG	4150
CAAGATGGAA	ACGCAGAAAA	TGAACCGGGG	ATGCGACGTG	CAAGATTACC	4200
TATGCAATAG	ATGCAATAGT	TTCTCCAGGA	ACCGAAATAC	ATACATTGTC	4250
TTCCGTAAAG	CGCTAGACTA	TATATTATTA	TACAGGTTCA	AATATACTAT	4300
CTGTTTCAGG	GAAAACCTCCC	AGGTTCGGAT	GTTCAAAATT	CAATGATGGG	4350
TAACAAGTAC	GATCGTAAAT	CTGTAAAACA	GTTCGCGGA	TATTAGGCTG	4400

TATCTCCTCA	AAGCGTATT	GAATATCATT	GAGAAGCTGC	ATTTTTTTT	4450
TTTTTTATAT	ATATTTCAG	GATATACCAT	TGTAATGCCT	GCCCCTAAGA	4500
AGATCGTCGT	TTTGCCAGGT	GACCACGTTG	GTCAAGAAAT	CACAGCCGAA	4550
GCCATTAAGG	TTCTTAAAGC	TATTCTGAT	GTTCGTTCCA	ATGTCAAGTT	4600
CGATTTGAA	AATCATTAA	TTGGTGGTGC	TGCTATCGAT	GCTACAGGTG	4650
TTCCACTTCC	AGATGAGGCC	CTGGAAGCCT	CCAAGAAGGC	TGATGCCGTT	4700
TTGTTAGGTG	CTGTGGGTGG	TCCTAAATGG	GGTACCGGTA	GTGTTAGACC	4750
TGAACAAGGT	TTACTAAAAA	TCCGTAAGA	ACTTCAATTG	TACGCCAATC	4800
TAAGACCATG	TAACCTTGCA	TCCGACTCTC	TTTAGACTT	ATCTCCAATC	4850
AAGCCACAAT	TTGCTAAAGG	TACTGACTTC	GTTGTTGTTA	GAGAATTAGT	4900
GGGAGGTATT	TACTTGGTA	AGAGAAAAGGA	AGACGATGGT	GATGGTGTG	4950
CTTGGGATAG	TGAACAATAC	ACCGTTCCAG	AAGTGCAAAG	AATCACAAAGA	5000
ATGGCCGCTT	TCATGGCCCT	ACAACATGAG	CCACCATTGC	CTATTGGTC	5050
CTTGGATAAA	GCTAATGTTT	TGGCCTCTTC	AAGATTATGG	AGAAAAACTG	5100
TGGAGGAAAC	CATCAAGAAC	GAATTCCCTA	CATTGAAAGT	TCAACATCAA	5150
TTGATTGATT	CTGCCGCCAT	GATCCTAGTT	AAGAACCCAA	CCCACCTAAA	5200
TGGTATTATA	ATCACCCAGCA	ACATGTTGG	TGATATCATC	TCCGATGAAG	5250
CCTCCGTTAT	CCCAGGCTCC	TTGGGTTTGT	TGCCATCTGC	GTCCTTGGCC	5300
TCTTGCCAG	ACAAGAACAC	CGCATTGTT	TTGTACGAAC	CATGCCATGG	5350
TTCCGCTCCA	GATTGCCAA	AGAATAAGGT	CAACCCATTC	GCCACTATCT	5400
TGTCTGCTGC	AATGATGTTG	AAATTGTCAT	TGAACCTGCC	TGAAGAAGGT	5450
AAAGCCATTG	AAGATGCAGT	AAAAAAGTT	TTGGATGCAG	GTATCAGAAC	5500
TGGTGATTTA	GGTGGTTCCA	ACAGTACAC	CGAAGTCGGT	GATGCTGTG	5550
CCGAAGAAGT	TAAGAAAATC	CTTGCTTAAA	AAGATTCTCT	TTTTTTATGA	5600
TATTGTAACA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	5650
AAAAAAAAAA	AAAATGCAGC	GTCACATCGG	ATAATAATGA	TGGCAGCCAT	5700
TGTAGAAGTG	CCTTTGCAT	TTCTAGTCTC	TTTCTCGGTC	TAGCTAGTTT	5750
TACTACATCG	CGAAGATAGA	ATCTTAGATC	ACACTGCCTT	TGCTGAGCTG	5800
GATCAATAGA	GTAACAAAAG	AGTGGTAAGG	CCTCGTTAAA	GGACAAGGAC	5850
CTGAGCGGAA	GTGTATCGTA	CAGTAGACGG	AGTATACTAG	TATAGTCTAT	5900
AGTCCGTGGA	ATTCTCATGT	TTGACAGCTT	ATCATCGATA	AGCTAGCTTT	5950
CTAACTGATC	TATCAAAAC	TGAAAATTAC	ATTCTTGATT	AGGTTTATCA	6000
CAGGCCAAATG	TAATTGTGG	TATTTGCCG	TTCAAAATCT	GTAGAATT	6050
CTCATTGGTC	ACATTACAAAC	CTGAAAATAC	TTTATCTACA	ATCATACCAT	6100
TCTTAATAAC	ATGTCCTCTT	AATACTAGGA	TCAGGCATGA	ACGCATCACA	6150
GACAAAATCT	TCTTGACAAA	CGTCACAATT	GATCCCTCCC	CATCCGTTAT	6200
CACAATGACA	GGTGTCAATT	TGTGCTCTTA	TGGGACGATC	CTTATTACCG	6250
CTTTCATCCG	GTGATTGACC	GCCACAGAGG	GGCAGAGAGC	AATCATCACC	6300
TGCAAACCCCT	TCTATACACT	CACATCTACC	AGTGATCGAA	TTGCATTCA	6350
AAAACGTGTTT	GCATTAAAAA	ATAGGTAGCA	TACAATTAAA	ACATGGCGGG	6400
CATGTATCAT	TGCCCTTATC	TTGTGCAGTT	AGACCGAAT	TTTCAAGA	6450
AGTACCTTCA	AAGAATGGGG	TCTTATCTTG	TTTGCAAGT	ACCACTGAGC	6500
AGGATAATAA	TAGAAATGAT	AATATACTAT	AGTAGAGATA	ACGTGATGA	6550
CTTCCCATAC	TGTAATTGCT	TTTAGTTGTG	TATTTTGT	GTCAGT	6600
CTGTAATTCG	ATTAATT	TTTCTTTCC	TCTTTTATT	AACCTTAATT	6650
TTTATTTAG	ATTCTGACT	TCAACTCAAG	ACGCACAGAT	ATTATAACAT	6700
CTGCATAATA	GGCATTGCA	AGAATTACTC	GTGAGTAAGG	AAAGAGTGAG	6750
GAACATATCGC	ATACCTGCAT	TTAAAGATGC	CGATTGGC	GCGAATCCTT	6800
TATTTTGGCT	TCACCCCTCAT	ACTATTATCA	GGGCCAGAAA	AAGGAAGTGT	6850

TTCCCTCCTT	CTTGAATTGA	TGTTACCCCTC	ATAAAGCACG	TGGCCTCTTA	6900
TCGAGAAAGA	AATTACCGTC	GCTCGTGATT	TGTTTGCAAA	AAGAACAAAA	6950
CTGAAAAAAC	CCAGACACGC	TCGACTTCCT	GTCTTCCTAT	TGATTGCAGC	7000
TTCCAATTTC	GTCACACAAAC	AAGGCCCTAG	CGACGGCTCA	CAGGTTTTGT	7050
AACAAGCAAT	CGAAGGTTCT	GGAAATGGCGG	GGAAAGGGTT	TAGTACCAACA	7100
TGCTATGATG	CCCACGTGA	TCTCCAGAGC	AAAGTTCGTT	CGATCGTACT	7150
GTACTCTCTC	TCTTTCAAAC	AGAATTGTCC	GAATCGTGTG	ACAACAAACAG	7200
CCTGTTCTCA	CACACTCTT	TCTCTTAACC	AAGGGGGTGG	TTTAGTTTAG	7250
TAGAACCTCG	TGAAACTTAC	ATTTACATAT	ATATAAAACTT	GCATAAATTG	7300
GTCAATGGAA	GAAATACATA	TTTGGTCTTT	TCTAATTCGT	AGTTTTCAA	7350
GTTCTTAGAT	GCTTTCTTTT	TCTCTTTTTT	ACAGATCATC	AAGGAAGTAA	7400
TTATCTACTT	TTTACAACAA	ATACAAAAGA	TCTATGAGAT	TTCCTTCAAT	7450
TTTTACTGCA	GTTTTATTGCG	CAGCATCCTC	CGCATTAGCT	GCTCCAGTCA	7500
ACACTACAAC	AGAAGATGAA	ACGGCACAAA	TTCCGGCTGA	AGCTGTCATC	7550
GGTTACTTAG	ATTTAGAAGG	GGATTCGAT	GTTGCTGTTT	TGCCATTTTC	7600
CAACAGCACA	AATAACGGGT	TATTGTTAT	AAATACTACT	ATTGCCAGCA	7650
TTGCTGCTAA	AGAAGAAGGG	GTAAGCTTGG	ATAAAAGAAA	CAGCGACTCT	7700
GAATGCCCGC	TGAGCCATGA	TGGCTACTGC	CTGCACGACG	GTGTATGCAT	7750
GTATATCGAA	GCTCTGGACA	AATACGCATG	CAACTGCGTA	GTTGGTTACA	7800
TCGGCGAACG	TTGCCAGTAC	CGCGACCTGA	AATGGTGGGA	GCTCCGTTAA	7850
TAAGGATCC					7859

***** END OF SEQ ID NO: 4 *****

75

SEQ. ID NO:5

SEQUENCE TYPE: nucleotide

SEQUENCE LENGTH: 15 base pairs

FEATURES: Top strand of adapter to fuse C-terminal
end of the α -factor pro-peptide to
synthetic hirudin gene

SEQUENCE:

AGCTTGGATA AAAGA

15

***** END OF SEQ ID NO: 5 *****

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SEQ. ID NO:6

SEQUENCE TYPE: nucleotide

SEQUENCE LENGTH: 11 base pairs

FEATURES: Bottom strand of adapter to fuse C-terminal end of the α -factor pro-peptide to synthetic hirudin gene

SEQUENCE:

TCTTTATCC A

11

***** END OF SEQ ID NO: 6 *****

SUBSTITUTE SHEET

SEQ ID NO:7

SEQUENCE TYPE: nucleotide
SEQUENCE LENGTH: 223 base pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
SOURCE: synthetic
FEATURES: hirudin type HV-1 gene with 5 amino acid adaptor (corresponding to C-terminus of alpha factor) at amino terminus.
from 1 to 6 bp (AAGCTT) is HindIII site
from 118 to 123 bp (GGATCC) is BamHI site.

SEQUENCE:

AAGCTTGGAT	AAAAGAGTTG	TTTACACCGA	CTGTACTGAA	TCCGGACAAA	50
ACCTGTGTTT	GTGTGAGGGT	TCTAACGTCT	GTGGTCAGGG	TAACAAATGC	100
ATCCTGGGTT	CCGACGGTGA	AAAGAACCAA	TGTGTCACTG	GTGAAGGTAC	150
CCCAAAGCCG	CAGTCCCACA	ACGATGGAGA	TTTCGAAGAA	ATCCCAGAAG	200
AATATCTGCA	GTAATAGGGA	TCC			223

***** END OF SEQ ID NO: 7 *****

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SEQ ID NO:8

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 420 base pairs
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURES: Factor Xa-cleavable Hirudin-IEGR-Hirudin
 SEQUENCE:

GTT	GTT	TAC	ACC	GAC	TGT	ACT	GAA	TCC	GGA	CAA	AAC	CTG	TGT		42
Val	Val	Tyr	Thr	Asp	Cys	Thr	Glu	Ser	Gly	Gln	Asn	Leu	Cys		
					5								10		
TTG	TGT	GAG	GGT	TCT	AAC	GTC	TGT	GGT	CAG	GGT	AAC	AAA	TGC		84
Leu	Cys	Glu	Gly	Ser	Asn	Val	Cys	Gly	Gln	Gly	Asn	Lys	Cys		
15					20								25		
ATC	CTG	GGT	TCC	GAC	GGT	GAA	AAG	AAC	CAA	TGT	GTC	ACT	GGT		126
Ile	Leu	Gly	Ser	Asp	Gly	Glu	Lys	Asn	Gln	Cys	Val	Thr	Gly		
30					35								40		
GAA	GGT	ACC	CCA	AAG	CCG	CAG	TCC	CAC	AAC	GAT	GGA	GAT	TTC		168
Glu	Gly	Thr	Pro	Lys	Pro	Gln	Ser	His	Asn	Asp	Gly	Asp	Phe		
45					50								55		
GAA	GAA	ATC	CCA	GAA	GAA	TAT	CTG	CAG	ATC	GAA	GGA	AGA	GTT		210
Glu	Glu	Ile	Pro	Glu	Glu	Tyr	Leu	Gln	Ile	Glu	Gly	Arg	Val		
60					65								70		
GTT	TAC	ACC	GAC	TGT	ACT	GAA	TCC	GGA	CAA	AAC	CTG	TGT	TTG		252
Val	Tyr	Thr	Asp	Cys	Thr	Glu	Ser	Gly	Gln	Asn	Leu	Cys	Leu		
75					80										
TGT	GAG	GGT	TCT	AAC	GTC	TGT	GGT	CAG	GGT	AAC	AAA	TGC	ATC		294
Cys	Glu	Gly	Ser	Asn	Val	Cys	Gly	Gln	Gly	Asn	Lys	Cys	Ile		
85					90								95		
CTG	GGT	TCC	GAC	GGT	GAA	AAG	AAC	CAA	TGT	GTC	ACT	GGT	GAA		336
Leu	Gly	Ser	Asp	Gly	Glu	Lys	Asn	Gln	Cys	Val	Thr	Gly	Glu		
100					105								110		
GGT	ACC	CCA	AAG	CCG	CAG	TCC	CAC	AAC	GAT	GGA	GAT	TTC	GAA		378
Gly	Thr	Pro	Lys	Pro	Gln	Ser	His	Asn	Asp	Gly	Asp	Phe	Glu		
115					120								125		
GAA	ATC	CCA	GAA	GAA	TAT	CTG	CAG	TAATAGGGAT	CCGAATT						420
Glu	Ile	Pro	Glu	Glu	Tyr	Leu	Gln								
130															

***** END OF SEQ ID NO: 8 *****

SEQ. ID NO:13

SEQUENCE TYPE: nucleotide

SEQUENCE LENGTH: 17 base pairs

FEATURES: Primers for dideoxy sequencing of
streptokinase gene

SEQUENCE:

5'-CACTATCAGTAGCAAAT-3'	BB 3510
5'-TGGTCTAACGCGCACAT-3'	BB 2136
5'-GAGTAAACTGTACAGTA-3'	BB 3509
5'-GATCTCATAAGCTTGTT-3'	BB 3508
5'-TTTAGCCTTATCACGAG-3'	BB 2135
5'-GACACCAACCGTATCAT-3'	BB 2753
5'-CGTTGATGTCAACACCA-3'	BB 3718
5'-GCTATCGGTGACACCAT-3'	BB 2754
5'-GACGACTACTTGAGGT-3'	BB 2755
5'-CCCAACCTGTCCAAGAA-3'	BB 2134

***** END OF SEQ ID NO: 13 *****

SUBSTITUTE SHEET

SEQ. ID NO:14

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 1335 base pairs
 FEATURES: Streptokinase gene from S. equisimilis
 SEQUENCE:

GAATTCATGAAAAATTACTTATCTTTGGGATGTTGCACTGCTGTTGCACTAACATTT
 MetLysAsnTyrLeuSerPheGlyMetPheAlaLeuLeuPheAlaLeuThrPhe
 GGAACAGTCAATTCTGTCCAAGCTATTGCTGGACCTGAGTGGCTGCTAGACCCTCCATCT
 GlyThrValAsnSerValGlnAlaIleAlaGlyProGluTrpLeuLeuAspArgProSer
 GTCAACAAACAGCCAATTAGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAAGAC
 ValAsnAsnSerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAsp
 ATTAGTCTTAAATTTTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACA
 IleSerLeuLysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThr
 GAGCAAGGCTTAAGTCCAAAATCAAAACCATTGCTACTGATAGTGGCGCGATGCCACAT
 GluGlnGlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetProHis
 AAACCTGAAAAAGCTGACTTAAAGGCTATTCAAGAACAAATTGATCGCTAACGTCCAC
 LysLeuGluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHis
 AGTAACGACGACTACTTGAGGTCAATTGATTTGCAAGCGATGCAACCATTACTGATCGA
 SerAsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArg
 AACGGCAAGGTCTACTTGCTGACAAAGATGGTCGGTAACCTGCCAACCTGTC
 AsnGlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProVal
 CAAGAATTTTGCTAACGGACATGTGCGCGTTAGACCATAAAAGAAAAACCAATACAA
 GlnGluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGln
 AATCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTACTCCCTAAACCCCTGAT
 AsnGlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp
 GACGATTTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGAC
 AspAspPheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAsp
 ACCATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTAAACAAACCCATCCA
 ThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysThrHisPro
 GGCTATACGATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTCCGT
 GlyTyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArg
 ACGATTTACCAATGGATCAAGAGTTACTTACCATGTCAAAATCGGGAACAGCTTAT
 ThrIleLeuProMetAspGlnGluPheThrTyrHisValLysAsnArgGluGlnAlaTyr

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GAGATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAAACACTGACCTGATCTCTGAG
GluIleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGlu

AAATATTACGTCTTAAAAAGGGAAAAGCCGTATGATCCCTTGATCGCAGTCACTTG
LysTyrTyrValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeu

AAACTGTTACCACATCAAATACGTTGATGTCAACACCAACGAATTGCTAAAAAGCGAGCAG
LysLeuPheThrIleLysTyrValAspValAsnThrAsnGluLeuLeuLysSerGluGln

CTCTTAACAGCTAGCGAACGTAACCTAGACTTCAGAGATTATACGATCCTCGTGATAAG
LeuLeuThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLys

GCTAAACTACTCTACAACAATCTCGATGCTTTGGTATTATGGACTATACTTAACTGGAA
AlaLysLeuLeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGly

AAAGTAGAAGATAATCACGATGACACCAACCGTATCATAACCGTTATATGGCAAGCGA
LysValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArg

CCCGAAGGAGAGAATGCTAGCTATCATTAGCCTATGATAAAAGATCGTTACCGAAGAA
ProGluGlyGluAsnAlaSerTyrHisLeuAlaTyrAspLysAspArgTyrThrGluGlu

GAACGAGAAGTTACAGCTACCTGCCTTATACAGGGACACCTATACCTGATAACCTAAC
GluArgGluValTyrSerTyrLeuArgTyrThrGlyThrProIleProAspAsnProAsn

GACAAATAAGGATCC*
AspLysEnd

***** END OF SEQ ID NO: 14 *****

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SEQ. ID NO:17

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 1317 base pairs
 FEATURES: OmpAL fused to mature streptokinase gene
 SEQUENCE:

CATATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTCGCGACCGTAGCG
 M K K T A I A I A V A L A G F A T V A
 CAGGCCATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAAACAGCCAATTA
 Q A I A G P E W L L D R P S V N N S Q L
 GTTGTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTT
 V V S V A G T V E G T N Q D I S L K F F
 GAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCA
 E I D L T S R P A H G G K T E Q G L S P
 AAATCAAAACCATTGCTACTGATAGTGGCGCGATGCCACATAAACTTGAAAAAGCTGAC
 K S K P F A T D S G A M P H K L E K A D
 TTACTAAAGGCTATTCAAGAACAAATTGATCGCTAACGTCCACAGTAACGACGACTACTTT
 L L K A I Q E Q L I A N V H S N D D Y F
 GAGGTCAATTGATTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTT
 E V I D F A S D A T I T D R N G K V Y F
 GCTGACAAAGATGGTCGTAACCTGCCGACCCAACCTGTCCAAGAATTGGCTAACGC
 A D K D G S V T L P T Q P V Q E F L L S
 GGACATGTGCGCGTTAGACCATATAAGAAAAACCAATAACAAATCAAGCGAAATCTGTT
 G H V R V R P Y K E K P I Q N Q A K S V
 GATGTGGAATATACTGTACAGTTACTCCCTTAAACCTGATGACGATTCAGACCAAGGT
 D V E Y T V Q F T P L N P D D D F R P G
 CTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAA
 L K D T K L L K T L A I G D T I T S Q E
 TTACTAGCTCAAGCACAAAGCATTAAACAAACCCATCCAGGCTATACGATTTATGAA
 L L A Q A Q S I L N K T H P G Y T I Y E
 CGTGACTIONCTCAATCGTCACTCATGACAATGACATTTCGGTACGATTTACCAATGGAT
 R D S S I V T H D N D I F R T I L P M D
 CAAGAGTTACTTACCATGTAAAAATCGGGAACAGCTTATGAGATCAATAAAAATCT
 Q E F T Y H V K N R E Q A Y E I N K K S

SUBSTITUTE SHEET

GGTCTGAATGAAGAAATAAACAAACACTGACCTGATCTCTGAGAAATATTACGTCCCTAAA
G L N E E I N N T D L I S E K Y Y V L K

AAAGGGGAAAAGCCGTATGATCCCTTGATCGCAGTCACTTGAAACTGTTACCATCAAA
K G E K P Y D P F D R S H L K L F T I K

TACGTTGATGTCAACACCAACGAATTGCTAAAAAGCGAGCAGCTCTTAACAGCTAGCGAA
Y V D V N T N E L L K S E Q L L T A S E

CGTAACTTAGACTTCAGAGATTATACGATCCTCGTGATAAGGCTAAACTACTCTACAAC
R N L D F R D L Y D P R D K A K L L Y N

AATCTCGATGCTTTGGTATTATGGACTATACCTTAACGGAAAAGTAGAAGATAATCAC
N L D A F G I M D Y T L T G K V E D N H

GATGACACCAACCGTATCATAACGTTATATGGCAAGCGACCCGAAGGAGAGAATGCT
D D T N R I I T V Y M G K R P E G E N A

AGCTATCATTAGCCTATGATAAAAGATCGTTATACCGAAGAAGAACGAGAAGTTACAGC
S Y H L A Y D K D R Y T E E E R E V Y S

TACCTGCCTTATACAGGGACACCTATACTGATAACCCTAACGACAAATAAGGATCC*
Y L R Y T G T P I P D N P N D K *

***** END OF SEQ ID NO: 17 *****

SUBSTITUTE SHEET

SEQ. ID NO:23

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 1197 nucleotides
 FEATURES: Methionyl-streptokinase fusion protein
 SEQUENCE:

CATATGATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAACAGCCAATT
 MetIleAlaGlyProGluTrpLeuLeuAsnArgProSerValAsnAsnSerGlnLeu
 GTTGTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATT
 ValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeuLysPhePhe
 GAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCA
 GluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerPro
 AAATCAAAACCATTGCTACTGATAGTGGCGCGATGCCACATAAACTTGAAAAAGCTGAC
 LysSerLysProPheAlaThrAspSerGlyAlaMetProHisLysLeuGluLysAlaAsp
 TTACTAAAGGCTATTCAAGAACATTGATCGCTAACGTCCACAGTAACGACGACTACTTT
 LeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPhe
 GAGGTCATTGATTTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTT
 GluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPhe
 GCTGACAAAGATGGTCGGTAACCTGCCGACCCAACCTGTCCAAGAATTGCTAAGC
 AlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSer
 GGACATGTGCGCGTTAGACCATAAAAGAAAAACCAATAACAAATCAAGCGAAATCTGTT
 GlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAlaLysSerVal
 GATGTGGAATATACTGTACAGTTACTCCCTAAACCTGATGACGATTTCAGACCAGGT
 AspValGluTyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGly
 CTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCACATCTCAAGAA
 LeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGlu
 TTACTAGCTCAAGCACAAAGCATTAAACAAACCCATCCAGGCTATACGATTGAA
 LeuLeuAlaGlnAlaGlnSerIleLeuAsnLysThrHisProGlyTyrThrIleTyrGlu
 CGTGAECTCCTCAATCGTCACTCATGACAATGACATTTCGGTACGATTACCAATGGAT
 ArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAsp
 CAAGAGTTTACTTACCATGTAAAAATCGGGAACAAAGCTTATGAGATCAATAAAATCT
 GlnGluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGluIleAsnLysSer
 GGTCTGAATGAAGAAATAAACACTGACCTGATCTCTGAGAAATATTACGTCCTTAAA
 GlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLys

SUBSTITUTE SHEET

AAAGGGAAAAGCCGTATGATCCCTTGATCGCAGTCATTGAACTGTTACCATCAAA
LysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLys
TACGTTGATGTCAACACCAACGAATTGCTAAAAGCGAGCAGCTCTAACAGCTAGCGAA
TyrValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGlu
CGTAACCTAGACTTCAGAGATTATACGATCCTCGTGATAAGGCTAACTACTCTACAAC
ArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsn
AATCTCGATGCTTTGGTATTATGGACTATACCTTAACGGAAAAGTAGAAGATAATCAC
AsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHis
GATGACACCAACCGTATCATAACC GTTATATGGCAAGCGACCCGAAGGAGAGAATGCT
AspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAla
AGCTATCATTAGCCTATGATAAAAGATCGTTATACCGAAGAACGAGAAAGTTACAGC
SerTyrHisLeuAlaTyrAspLysAspArgTyrThrGluGluGluArgGluValTyrSer
TACCTGC GTTATACAGGGACACCTATACCTGATAACCCTAACGACAAATAAGGATCC*
TyrLeuArgTyrThrGlyThrProIleProAspAsnProAsnAspLysEnd

***** END OF SEQ ID NO: 23 *****

SUBSTITUTE SHEET

SEQ. ID NO:24

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 1513 nucleotides
 FEATURES: Streptokinase fused to yeast α -factor
 SEQUENCE:

AGATCTATGAGATTCTCAATTTACTGCAGTTTATTGCAGCATCCTCCGCATTA
 MetArgPheProSerIlePheThrAlaValLeuPheAlaAlaSerSerAlaLeu
 GCTGCTCCAGTCAACACTACAACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTC
 AlaAlaProValAsnThrThrGluAspGluThrAlaGlnIleProAlaGluAlaVal
 ATCGGTTACTTAGATTAGAAGGGGATTCGATGTTGCTGTTGCCATTTCCAACAGC
 IleGlyTyrLeuAspLeuGluGlyAspPheAspValAlaValLeuProPheSerAsnSer
 ACAAAATAACGGGTTATTGTTATAAAACTACTATTGCCAGCATTGCTGCTAAAGAACAGA
 ThrAsnAsnGlyLeuLeuPheIleAsnThrThrIleAlaSerIleAlaAlaLysGluGlu
 GGGGTAAGCTTGGATAAAAGAATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTC
 GlyValSerLeuAspLysArgIleAlaGlyProGluTrpLeuLeuAspArgProSerVal
 AACAAACAGCCAATTAGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATT
 AsnAsnSerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIle
 AGTCTTAAATTTTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAG
 SerLeuLysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGlu
 CAAGGCTTAAGTCCAAAATCAAACCATTGCTACTGATAGTGGCGCGATGCCACATAAA
 GlnGlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetProHisLys
 CTTGAAAAAGCTGACTTAAAGGCTATTCAAGAACATTGATCGCTAACGTCCACAGT
 LeuGluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSer
 AACCGACGACTACTTGAGGTCTTGCAAGCGATGCAACCATTACTGATCGAAAC
 AsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsn
 GGCAAGGTCTACTTGCTGACAAAGATGGTCGGTAACCTGCCGACCCAACCTGTCCAA
 GlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGln
 GAATTTTGCTAAGCGGACATGTGCGCGTTAGACCATATAAAGAAAAACCAATAACAAAAT
 GluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsn
 CAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTACTCCCTTAAACCTGATGAC
 GlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAsp
 GATTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACC
 AspPheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThr

ATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTTAACAAAACCCATCCAGGC
IleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysThrHisProGly

TATACGATTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTCGGTACG
TyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThr

ATTTTACCAATGGATCAAGAGTTACTTACCATGTCAAAAATCGGAACAAGCTTATGAG
IleLeuProMetAspGlnGluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGlu

ATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAACTGACCTGATCTCTGAGAAA
IleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLys

TATTACGTCTTAAAAAGGGAAAAGCCGTATGATCCCTTGATCGCAGTCACTGAAA
TyrTyrValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLys

CTGTTCACCATCAAATACGTTGATGTCAACACCAACGAATTGCTAAAAGCGAGCAGCTC
LeuPheThrIleLysTyrValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeu

TTAACAGCTAGCGAACGTAACCTAGACTTCAGAGATTATCGATCCTCGTGATAAGGCT
LeuThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAla

AAACTACTCTACAACAATCTCGATGCTTTGGTATTATGGACTATACCTTAACGGAAAAA
LysLeuLeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLys

GTAGAAGATAATCACGATGACACCAACCGTATCATAACCGTTATGGCAAGCGACCC
ValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgPro

GAAGGGAGAGAATGCTAGCTATCATTAGCCTATGATAAAGATCGTTATACCGAAGAAGAA
GluGlyGluAsnAlaSerTyrHisLeuAlaTyrAspLysAspArgTyrThrGluGluGlu

CGAGAAGTTACAGCTACCTCGCTTATACAGGGACACCTATACCTGATAACCCTAACGAC
ArgGluValTyrSerTyrLeuArgTyrThrGlyThrProIleProAspAsnProAsnAsp

AAATAAGGATCC*
LysEnd

***** END OF SEQ ID NO: 24 *****

SUBSTITUTE SHEET

SEQ. ID NO:26

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 1120 nucleotides
 FEATURES: Truncated Met-streptokinase (aa 16-383)
 SEQUENCE:

CATATGAGCCAATTAGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATT
 MetSerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIle
 AGTCTTAAATTTTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAG
 SerLeuLysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGlu
 CAAGGCTTAAGTCCAAAATCAAACCAATTGCTACTGATAGTGGCGCGATGCCACATAAA
 GlnGlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetProHisLys
 CTTGAAAAAGCTGACTTAAAGGCATTCAAGAACAAATTGATCGCTAACGTCCACAGT
 LeuGluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSer
 AACGACGACTACTTGAGGTCAATTGATTTGCAAGCGATGCAACCATTACTGATCGAAAC
 AsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsn
 GGCAAGGTCTACTTGCTGACAAAGATGGTCGGTAACCTGCCAACCTGTCCAA
 GlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGln
 GAATTTTGCTAAGCGGACATGTGCGCGTAGACCATAAAGAAAAACCAATACAAAAT
 GluPheLeuLeuSerGlyHisValArgProTyrLysGluLysProIleGlnAsn
 CAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTACTCCCTAAACCTGATGAC
 GlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAsp
 GATTCAGACCAGGTCTCAAAGATACTAACGCTATTGAAAACACTAGCTATCGGTGACACC
 AspPheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThr
 ATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTAAACAAAACCCATCCAGGC
 IleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysThrHisProGly
 TATACGATTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTCGGTACG
 TyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThr
 ATTTTACCAATGGATCAAGAGTTACTTACCATGTCAAAATCGGGAAACAAGCTTATGAG
 IleLeuProMetAspGlnGluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGlu
 ATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAAACACTGACCTGATCTCTGAGAAA
 IleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLys
 TATTACGTCCCTTAAAAAGGGAAAAGCCGTATGATCCCTTGATCGCAGTCACTTGAAA
 TyrTyrValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLys

SUBSTITUTE SHEET

CTGTTACCATCAAATACGTTGATGTCAACACCAACGAATTGCTAAAAGCGAGCAGCTC
LeuPheThrIleLysTyrValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeu
TTAACAGCTAGCGAACGTAACCTAGACTTCAGAGATTATACGATCCTCGTGATAAGGCT
LeuThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAla
AAACTACTCTACAACAATCTCGATGCTTTGGTATTATGGACTATACCTTAACGGAAAAA
LysLeuLeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLys
GTAGAAGATAATCACGATGACACCAACCGTATCATAACCGTTATATGGGCAAGCGACCC
ValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgPro
GAAGGAGAGAATGCTAGCTATCATTAGCCTAAGGATCC*
GluGlyGluAsnAlaSerTyrHisLeuAlaEnd

***** END OF SEQ ID NO: 26 *****

SUBSTITUTE SHEET

SEQ. ID NO:29

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 2590 nucleotides
 FEATURES: OmpAL-Streptokinase-streptokinase fusion
 linked by thrombin-cleavable VELQGVVPRG
 SEQUENCE:

CATATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTCGCGACCGTAGCG
 MetLysLysThrAlaIleAlaIleAlaValAlaLeuAlaGlyPheAlaThrValAla
 CAGGCCATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAAACAGCCAATT
 GlnAlaIleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeu
 GTTGTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTT
 ValValSerValAlaGlyThrValGluglyThrAsnGlnAspIleSerLeuLysPhePhe
 GAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCA
 GluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerPro
 AAATCAAAACCATTGCTACTGATAGTGGCGCGATGCCACATAAAACTTGAAAAAGCTGAC
 LysSerLysProPheAlaThrAspSerGlyAlaMetProHisLysLeuGluLysAlaAsp
 TTACTAAAGGCTATTCAAGAACATTGATCGCTAACGTCCACAGTAACGACGACTACTTT
 LeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspAspTyrPhe
 GAGGTCAATTGATTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAGGTCTACTTT
 GluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPhe
 GCTGACAAAGATGGTCGGTAACCTGCCGACCCAACCTGTCCAAGAATTGGCTAAGC
 AlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSer
 GGACATGTGCGCGTTAGACCATATAAGAAAAACCAATAACAAATCAAGCGAAATCTGTT
 GlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAlaLysSerVal
 GATGTGGAATATACTGTACAGTTACTCCCTAAACCTGATGACGATTCAGACCAGGT
 AspValGluTyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGly
 CTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATCACATCTCAAGAA
 LeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGlu
 TTACTAGCTCAAGCACAAAGCATTAAACAAACCCATCCAGGCTATACGATTTATGAA
 LeuLeuAlaGlnAlaGlnSerIleLeuAsnLysThrHisProGlyTyrThrIleTyrGlu
 CGTGACTIONCTCAATCGTCACTCATGACAATGACATTCCAGGCTACGATTTACCAATGGAT
 ArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAsp
 CAAGAGTTTACTTACCATGTAAAAATCGGGAACAGCTTATGAGATCAATAAAATCT
 GlnGluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGluIleAsnLysSer

SUBSTITUTE SHEET

GGTCTGAATGAAGAAATAAACAAACACTGACCTGATCTCTGAGAAATATTACGTCCCTAAA
GlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLys
AAAGGGGAAAAGCCGTATGATCCCTTGATCGCAGTCACTTGAAACTGTTCACCATCAAA
LysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLys
TACGTTGATGTCAACACCAACGAATTGCTAAAAAGCGAGCAGCTTAACAGCTAGCGAA
TyrValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGlu
CGTAACCTAGACTTCAGAGATTATACGATCCTCGTGATAAGGCTAAACTACTCTACAAC
ArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsn
AATCTCGATGCTTTGGTATTATGGACTATACTTAACGGAAAAGTAGAAGATAATCAC
AsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHis
GATGACACCAACCGTATCATAACCGTTATATGGGCAAGCGACCCGAAGGAGAGAATGCT
AspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAla
AGCTATCATTAGCCTATGATAAAGATCGTTACCGAAGAAGAACGAGAAGTTACAGC
SerTyrHisLeuAlaTyrAspLysAspArgTyrThrGluGluGluArgGluValTyrSer
TACCTGCCTTATACAGGGACACCTATACTGATAACCCTAACGACAAAGTAGAGCTGCAG
TyrLeuArgTyrThrGlyThrProIleProAspAsnProAspLysValGluLeuGln
GGAGTAGTTCCCTCGTGGATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAAC
GlyValValProArgGlyIleAlaGlyProGluTrpLeuLeuAspArgProSerValAsn
AACAGCCAATTAGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGT
AsnSerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSer
CTTAAATTTTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAA
LeuLysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGln
GGCTTAAGTCCAAATCAAACCATTGCTACTGATAGTGGCGCGATGCCACATAAACTT
GlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetProHisLysLeu
GAAAAAGCTGACTTACTAAAGGCTATTCAAGAACAAATTGATCGCTAACGTCCACAGTAAC
GluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsn
GACGACTACTTGAGGTATTGATTTGCAAGCGATGCAACCATTACTGATCGAAACGGC
AspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGly
AAGGTCTACTTGCTGACAAAGATGGTTGGTAACCTGCCGACCCAACCTGTCCAAGAA
LysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGlu
TTTTGCTAACGGGACATGTGCGCGTTAGACCATAAAAGAAAAACCAATACAAAATCAA
PheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGln

SUBSTITUTE SHEET

GCGAAATCTGTTGATGTGGAATATACTGTACAGTTACTCCCTAAACCCTGATGACGAT
 AlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspAsp
 TTCAGACCAGGTCTCAAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCATC
 PheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIle
 ACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTTAAACAAAACCATCCAGGCTAT
 ThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysThrHisProGlyTyr
 ACGATTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTCGTACGATT
 ThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIle
 TTACCAATGGATCAAGAGTTACTTACCATGTCAAAATCGGGAACAGCTTATGAGATC
 LeuProMetAspGlnGluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGluIle
 AATAAAAATCTGGCTGAATGAAGAAATAAACACACTGACCTGATCTCTGAGAAATAT
 AsnLysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyr
 TACGTCTTAAAAAGGGGAAAGCCGTATGATCCCTTGATCGCAGTCAC TGAAACTG
 TyrValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeu
 TTCACCATCAAATACGTTGATGTCAACACCAACGAATTGCTAAAAGCGAGCAGCTCTTA
 PheThrIleLysTyrValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeu
 ACAGCTAGCGAACGTAACTTAGACTTCAGAGATTATACGATCCTCGTGATAAGGCTAA
 ThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLys
 CTACTCTACAACAATCTCGATGCTTTGGTATTATGGACTATACCTTAACGGAAAAGTA
 LeuLeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysVal
 GAAGATAATACGATGACACCAACCGTATCATAACCGTTATATGGCAAGCGACCCGAA
 GluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGlu
 GGAGAGAATGCTAGCTATCATTAGCCTATGATAAGATCGTTACCGAAGAACGAA
 GlyGluAsnAlaSerTyrHisLeuAlaTyrAspLysAspArgTyrThrGluGluArg
 GAAGTTTACAGCTACCTCGCTTACAGGGACACCTACCTGATAACCTAACGACAAA
 GluValTyrSerTyrLeuArgTyrThrGlyThrProIleProAspAsnProAsnAspLys
 TAAGGATCC*
 End

***** END OF SEQ ID NO: 29 *****

SUBSTITUTE SHEET

SEQ. ID NO:33

SEQUENCE TYPE: nucleotide with corresponding amino acid
SEQUENCE LENGTH: 2254 nucleotides
FEATURES: Met-corestreptokinase-corestreptokinase
fusion linked by thrombin-cleavable
VELQGVVPRG

SEQUENCE:

CATATGAGCCAATTAGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATT
MetSerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIle
AGTCTTAAATTTTGAAATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAG
SerLeuLysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGlu
CAAGGCTTAAGTCCAAAATCAAACCATTGCTACTGATAGTAGTCGGCGCGATGCCACATAAA
GlnGlyLeuSerProLysSerProPheAlaThrAspSerGlyAlaMetProHisLys
CTTGAAAAAGCTGACTTAAAGGCTATTCAAGAACATTGATCGCTAACGTCCACAGT
LeuGluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSer
AACGACGACTACTTGAGGTCTTGATTTGCAAGCGATGCAACCATTACTGATCGAAAC
AsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsn
GGCAAGGTCTACTTGCTGACAAAGATGGTCGGTAACCTGCCGACCCAACCTGTCCAA
GlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGln
GAATTGGCTAAGCGGACATGTGCGCGTTAGACCATATAAGAAAACCAATACAAAAT
GluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsn
CAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTACTCCCTAAACCCCTGATGAC
GlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAsp
GATTCAGACCAGGTCTCAAAGATACTAAAGCTATTGAAAACACTAGCTATCGGTGACACC
AspPheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThr
ATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTAAACAAAACCCATCCAGGC
IleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysThrHisProGly
TATACGATTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTCCGTACG
TyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThr
ATTTTACCAATGGATCAAGAGTTACTTACCATGTCAAAATCGGGAACAAAGCTTATGAG
IleLeuProMetAspGlnGluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGlu
ATCAATAAAAATCTGGTCTGAATGAAGAAATAAACAAACACTGACCTGATCTCTGAGAAA
IleAsnLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLys

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TATTACGTCTTAAAAAGGGAAAAGCCGTATGATCCCTTGATCGCAGTCACGGAAA
 TyrTyrValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLys
 CTGTTCACCATCAAATACGTTGATGTCAACACCAACGAATTGCTAAAAAGCGAGCAGCTC
 LeuPheThrIleLysTyrValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeu
 TTAACAGCTAGCGAACGTAACCTAGACTTCAGAGATTATCGATCCTCGTGATAAGGCT
 LeuThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAla
 AAACTACTCTACAACAATCTCGATGCTTTGGTATTATGGACTATACCTAACTGGAAAAA
 LysLeuLeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLys
 GTAGAAGATAATCACGATGACACCAACCGTATCATAACCGTTATATGGCAAGCGACCC
 ValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgPro
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 GluGlyGluAsnAlaSerTyrHisLeuAlaValGluLeuGlnGlyValValProArgGly
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 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly
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 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetProHisLysLeuGlu
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 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp
 GACTACTTGAGGTCAATTGATTGCAAGCGATGCAACCATTACTGATCGAAACGGCAAG
 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys
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ATTTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTCCGTACGATTAA
IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu
CCAATGGATCAAGAGTTACTTACCATGTCAAAAATCGGAAACAAGCTTATGAGATCAAT
ProMetAspGlnGluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGluIleAsn
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LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr
GTCCTTAAAAAAGGGAAAAGCCGTATGATCCCTTGATCGCAGTCAC TTGAAACTGTTTC
ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe
ACCATCAAATACGTTGATGTCAACACCAACGAATTGCTAAAAGCGAGCAGCTCTTAACA
ThrIleLysTyrValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr
GCTAGCGAACGTAACCTAGACTTCAGAGATTATACGATCCTCGTGATAAGGCTAAACTA
AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu
CTCTACAACAAATCTGATGCTTTGGTATTATGGACTATACCTTAACGGAAAAGTAGAA
LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu
GATAATCACGATGACACCAACCGTATCATAACCGTTATATGGGCAAGCGACCCGAAGGA
AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly
GAGAATGCTAGCTATCATTAGCCTAAGGATCC
GluAsnAlaSerTyrHisLeuAlaEnd

***** END OF SEQ ID NO: 33 *****

SUBSTITUTE SHEET

SEQ. ID NO:35

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 1459 nucleotides
 FEATURES: Hirudin-streptokinase fusion
 linked by Factor Xa-cleavable IEGR
 SEQUENCE:

GTTGTTTACACCGACTGTACTGAATCCGGACAAAACCTGTGTTGTGAGGGTTCTAAC
 ValValTyrThrAspCysThrGluSerGlyGlnAsnLeuCysLeuCysGluGlySerAsn
 GTCTGTGGTCAGGGTAACAAATGCATCCTGGGTTCCGACGGTGAAAAGAACCAATGTGTC
 ValCysGlyGlnGlyAsnLysCysIleLeuGlySerAspGlyGluLysAsnGlnCysVal
 ACTGGTGAAGGTACCCCAAAGCCGCAGTCCCACAACGATGGAGATTCGAAGAAATCCA
 ThrGlyGluGlyThrProLysProGlnSerHisAsnAspGlyAspPheGluGluIlePro
 GAAGAATATCTGCAGATCGAAGGTAGAATTGCTGGACCTGAGTGGCTGCTAGACCGTCCA
 GluGluTyrLeuGlnIleGluGlyArgIleAlaGlyProGluTrpLeuLeuAspArgPro
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 ThrGluGlnGlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetPro
 CATAAACTTGAAAAAGCTGACTTAACTAAAGGCTATTCAAGAACAAATTGATCGCTAACGTC
 HisLysLeuGluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnVal
 CACAGTAACGACGACTACTTGAGGTCATTGATTTGCAAGCGATGCAACCATTACTGAT
 HisSerAsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAsp
 CGAAACGGCAAGGTCTACTTGCTGACAAAGATGGTTCGGTAACCTGCCGACCCAACCT
 ArgAsnGlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnPro
 GTCCAAGAATTGGCTAACGGACATGTGCGCGTTAGACCATATAAGAAAAACCAATA
 ValGlnGluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIle
 CAAAATCAAGCGAAATCTGTTGATGTGGAATATACTGTACAGTTACTCCCTAACCCCT
 GlnAsnGlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnPro
 GATGACGATTTCAGACCAGGTCTCAAAGATACTAACGCTATTGAAAACACTAGCTATCGGT
 AspAspAspPheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGly

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GACACCATCACATCTCAAGAATTACTAGCTCAAGCACAAAGCATTAAACAAAACCAT
AspThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysThrHis

CCAGGCTATACTGATTATGAACGTGACTCCTCAATCGTCACTCATGACAATGACATTTC
ProGlyTyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePhe

CGTAGCATTACCAATGGATCAAGAGTTACTTACCATGTCAAAATCGGAAACAAGCT
ArgThrIleLeuProMetAspGlnGluPheThrTyrHisValLysAsnArgGluGlnAla

TATGAGATCAATAAAAAATCTGGTCTGAATGAAGAAATAAACAAACTGACCTGATCTCT
TyrGluIleAsnLysSerGlyLeuAsnGluIleAsnAsnThrAspLeuIleSer

GAGAAATATTACGTCTTAAAAAGGGAAAAGCCGTATGATCCCTTGATCGCAGTCAC
GluLysTyrTyrValLeuLysGlyGluLysProTyrAspProPheAspArgSerHis

TTGAAACTGTTACCATCAAATACGTTGATGTCAACACCAACGAATTGCTAAAAAGCGAG
LeuLysLeuPheThrIleLysTyrValAspValAsnThrAsnGluLeuLeuLysSerGlu

CAGCTCTAACAGCTAGCGAACGTAACCTAGACTTCAGAGATTACGATCCTCGTGAT
GlnLeuLeuThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAsp

AAGGCTAAACTACTCTACAACAATCTCGATGCTTGGTATTATGGACTATACTTAAC
LysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThr

GGAAAAGTAGAAGATAATCACCGATGACACCAACCGTATCATAACCGTTATATGGCAAG
GlyLysValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLys

CGACCCGAAGGAGAGAATGCTAGCTATCATTAGCCTATGATAAAAGATCGTTATACCGAA
ArgProGluGlyGluAsnAlaSerTyrHisLeuAlaTyrAspLysAspArgTyrThrGlu

GAAGAACGAGAAGTTACAGCTACCTGCGTTATACAGGGACACCTATACCTGATAACCCT
GluGluArgGluValTyrSerTyrLeuArgTyrThrGlyThrProIleProAspAsnPro

AACGACAAATAAGGATCC*
AsnAspLysEnd

***** END OF SEQ ID NO: 35 *****

SUBSTITUTE SHEET

SEQ. ID NO:38

SEQUENCE TYPE: nucleotide with corresponding amino acid
 SEQUENCE LENGTH: 1468 nucleotides
 FEATURES: Streptokinase-hirudin fusion
 linked by Factor Xa-cleavable IEGR
 SEQUENCE:

ATTGCTGGACCTGAGTGGCTGCTAGACCGTCCATCTGTCAACAAACAGCCAATTAGTT
 IleAlaGlyProGluTrpLeuLeuAspArgProSerValAsnAsnSerGlnLeuVal
 GTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTTAAATTTTGAA
 ValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeuLysPhePheGlu
 ATTGACCTAACATCACGACCTGCTCATGGAGGAAAGACAGAGCAAGGCTTAAGTCCAAA
 IleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGlyLeuSerProLys
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 SerLysProPheAlaThrAspSerGlyAlaMetProHisLysLeuGluLysAlaAspLeu
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 ValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyrPheAla
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 AspLysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeuSerGly
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 GTGGAATATACTGTACAGTTACTCCCTTAAACCTGATGACGATTCAGACCAGGTCTC
 ValGluTyrThrValGlnPheThrProLeuAsnProAspAspAspPheArgProGlyLeu
 AAAGATACTAAGCTATTGAAAACACTAGCTATCGGTGACACCACATCTCAAGAATT
 LysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeu
 CTAGCTCAAGCACAAAGCATTAAACAAACCCATCCAGGCTATCGATTATGAAACGT
 LeuAlaGlnAlaGlnSerIleLeuAsnLysThrHisProGlyTyrThrIleTyrGluArg
 GACTCCTCAATCGTCACTCATGACAATGACATTTCGGTACGATTTACCAATGGATCAA
 AspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGln
 GAGTTTACTTACCATGTCAAAAATCGGAAACAAGCTATGAGATCAATAAAAATCTGGT
 GluPheThrTyrHisValLysAsnArgGluGlnAlaTyrGluIleAsnLysSerGly

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CTGAATGAAGAAATAAACAAACACTGACCTGATCTCTGAGAAATATTACGTCTTAAAAAA
LeuAsnGluGlulleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLys

GGGGAAAAGCCGTATGATCCCTTGATCGCAGTCACTTGAAACTGTTACCACATCAAATAC
GlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyr

GTTGATGTCAACACCAACGAATTGCTAAAAGCGAGCAGCTCTAACAGCTAGCGAACGT
ValAspValAsnThrAsnGluLeuLeuLysSerGluGlnLeuLeuThrAlaSerGluArg

AACTTAGACTTCAGAGATTATACGATCCTCGTGATAAGGCTAAACTACTCTACAACAAT
AsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsn

CTCGATGCTTTGGTATTATGGACTATACCTTAACGGAAAGTAGAAGATAATCACGAT
LeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHisAsp

GACACCAACCGTATCATAACCGTTATATGGGCAAGCGACCCGAAGGAGAGAATGCTAGC
AspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAlaSer

TATCATTAGCCTATGATAAGATCGTTACCGAAGAACGAGAAGTTACAGCTAC
TyrHisLeuAlaTyrAspLysAspArgTyrThrGluGluArgGluValTyrSerTyr

CTGCGTTATACAGGGACACCTATACCTGATAACCTAACGACAAAATCGAAGGTAGAGTT
LeuArgTyrThrGlyThrProIleProAspAsnProAsnAspLysIleGluGlyArgVal

GTTTACACCGACTGTACTGAATCCGGACAAACCTGTGTTGTGAGGGTTCTAACGTC
ValTyrThrAspCysThrGluSerGlyGlnAsnLeuCysLeuCysGluGlySerAsnVal

TGTGGTCAGGGTAACAAATGCATCCTGGGTTCCGACGGTGAAAAGAACCAATGTGTC
CysGlyGlnGlyAsnLysCysIleLeuGlySerAspGlyGluLysAsnGlnCysValThr

GGTGAAGGTACCCCAAAGCCGCAGTCCCACAAACGATGGAGATTCGAAGAAATCCCAGAA
GlyGluGlyThrProLysProGlnSerHisAsnAspGlyAspPheGluGluIleProGlu

GAATATCTGCAGTAATAGGGATCCGAATTC*
GluTyrLeuGlnEndEnd

***** END OF SEQ ID NO: 38 *****

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CLAIMS

1. A fusion protein comprising a first sequence and a second sequence, the fusion protein being cleavable between the first and second sequences by an enzyme involved in blood clotting, wherein after the fusion protein is so cleaved the first and second sequences, or either of them, has greater fibrinolytic and/or anti-thrombotic activity than the uncleaved fusion protein.
2. A fusion protein as claimed in claim 1, which is a cleavable dimer of two fibrinolytic and/or anti-thrombotic proteins.
3. A fusion protein as claimed in claim 1 or 2, wherein the first sequence corresponds to a hirudin or to a protein having the activity of hirudin.
4. A fusion protein as claimed in claim 1 or 2, wherein the first sequence corresponds to streptokinase or to a protein having the activity of streptokinase.
5. A fusion protein as claimed in any one of claims 1 to 4, wherein the second sequence corresponds to a hirudin or to a protein having the activity of hirudin.
6. A fusion protein as claimed in any one of claims 1 to 4, wherein the second sequence corresponds to streptokinase or to a protein having the activity of streptokinase.

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7. A fusion protein as claimed in any one of claims 1 to 6, wherein the enzyme involved in blood clotting is kallikrein, Factor XIIa, XIa, IXa, VIIa, Xa, thrombin (Factor IIa) or activated protein C.
8. A fusion protein as claimed in any one of claims 1 to 6, wherein the enzyme involved in blood clotting is Factor Xa or thrombin.
9. A fusion protein as claimed in any one of claims 1 to 6, wherein the enzyme involved in blood clotting is Factor Xa.
10. A fusion protein as claimed in claim 9, comprising the cleavage site sequence P4-P3-Gly-Arg, wherein P4 represents a hydrophobic residue and P3 represents an acidic residue.
11. A fusion protein as claimed in claim 10, wherein the hydrophobic residue is isoleucine.
12. A fusion protein as claimed in any one of claims 1 to 6, wherein the enzyme involved in blood clotting is thrombin.
13. A fusion protein as claimed in claim 12, comprising the cleavage site sequence P4-P3-Pro-Arg-P1'-P2', wherein each of P4 and P3 independently represents a hydrophobic residue and each of P1' and P2' independently represents a non-acidic residue.

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14. A fusion protein as claimed in claim 12, comprising the cleavage site sequence P2-Arg-P1', wherein one of the residues P2 and P1' represents glycine, and the other is any amino acid residue.
15. A fusion protein as claimed in claim 12, comprising the cleavage site sequence Gly-Pro-Arg.
16. A process for the preparation of a fusion protein as claimed in any one of claims 1 to 15, the process comprising coupling successive amino acid residues together and/or ligating oligo- and/or poly-peptides.
17. Synthetic or recombinant nucleic acid coding for a fusion protein as claimed in any one of claims 1 to 15.
18. Nucleic acid as claimed in claim 17, which is a vector.
19. A process for the preparation of nucleic acid as claimed in claim 17, the process comprising coupling successive nucleotides together and/or ligating oligo- and/or poly-nucleotides.
20. A cell or cell line transformed or transfected with a vector as claimed in claim 18.
21. A cell as claimed in claim 20, which is a yeast cell.
22. A yeast cell as claimed in claim 21 which is Pichia pastoris or Saccharomyces cerevisiae.

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23. A cell as claimed in claim 20, which is a bacterial cell.
24. A bacterial cell as claimed in claim 23, which is Escherichia coli.
25. A pharmaceutical composition comprising one or more compounds as claimed in any one of claims 1 to 15 and a pharmaceutically or veterinarily acceptable carrier.
26. A method for the treatment or prophylaxis of thrombotic disease, the method comprising the administration of an effective, non-toxic amount of a fusion protein as claimed in any one of claims 1 to 15.
27. A proteinaceous compound as claimed in any one of claims 1 to 15 for use in human or veterinary medicine.
28. The use of a fusion protein as claimed in any one of claims 1 to 15 in the preparation of a thrombolytic and/or antithrombotic agent.

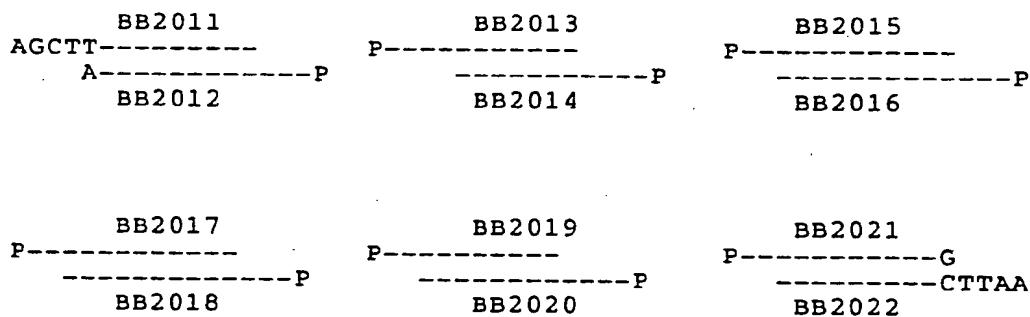
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FIG. 1.

SUMMARY OF ASSEMBLY PROCEDURE

The kinased oligomers were annealed in pairs. The oligomers BB2011 and BB2020 were not kinased to prevent multimerization.

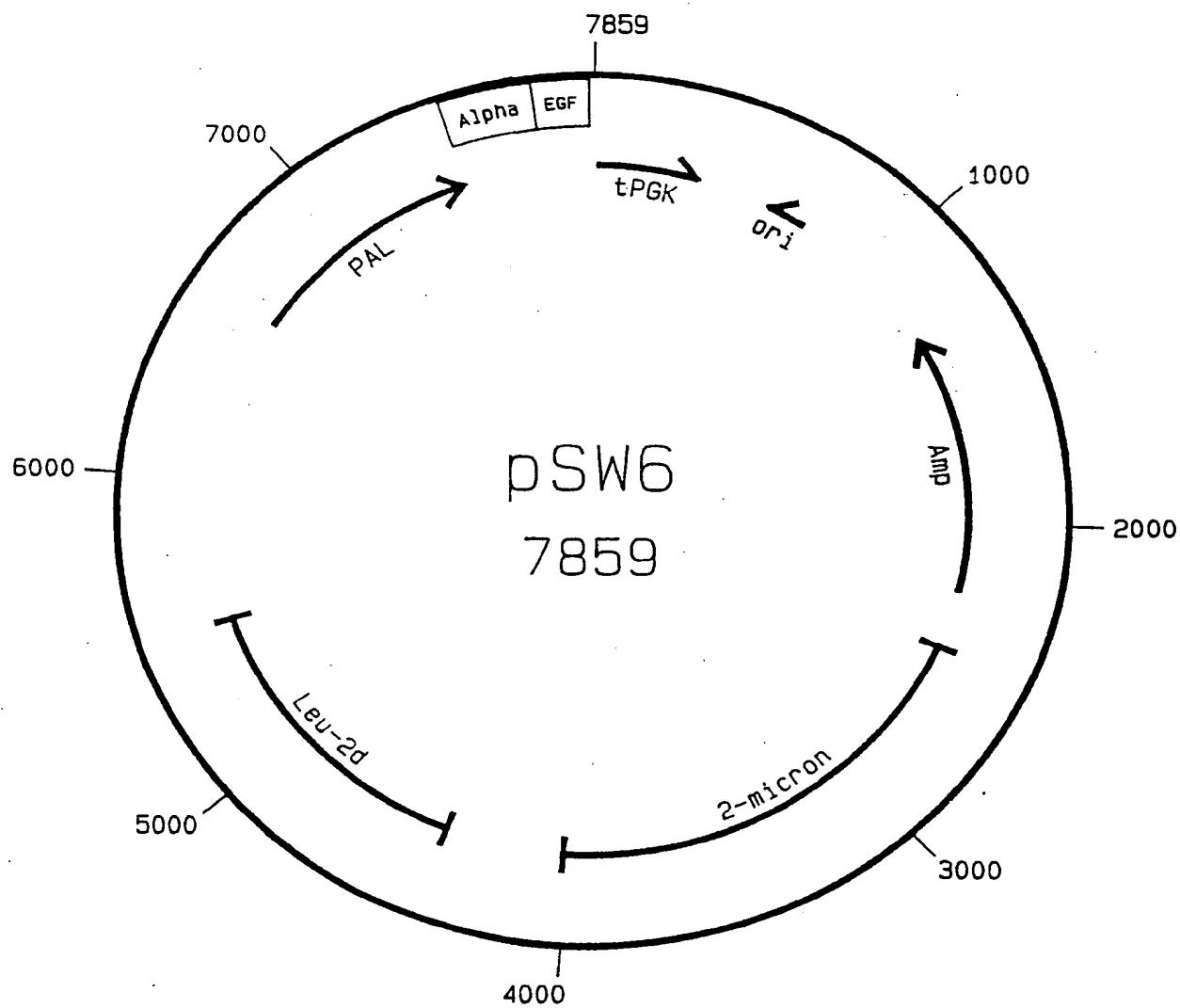


p=5' phosphate

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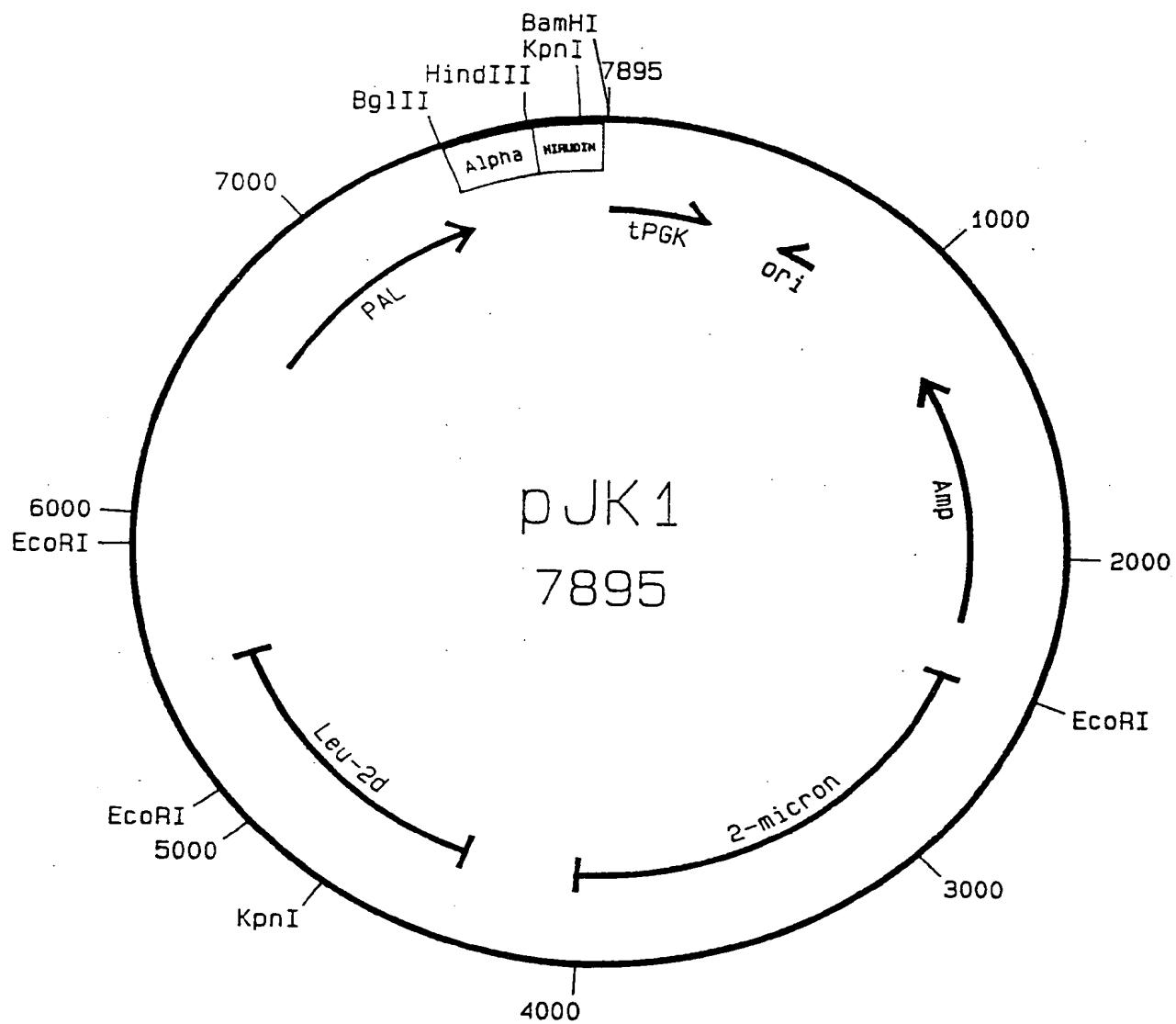
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FIG. 2.

**SUBSTITUTE SHEET**

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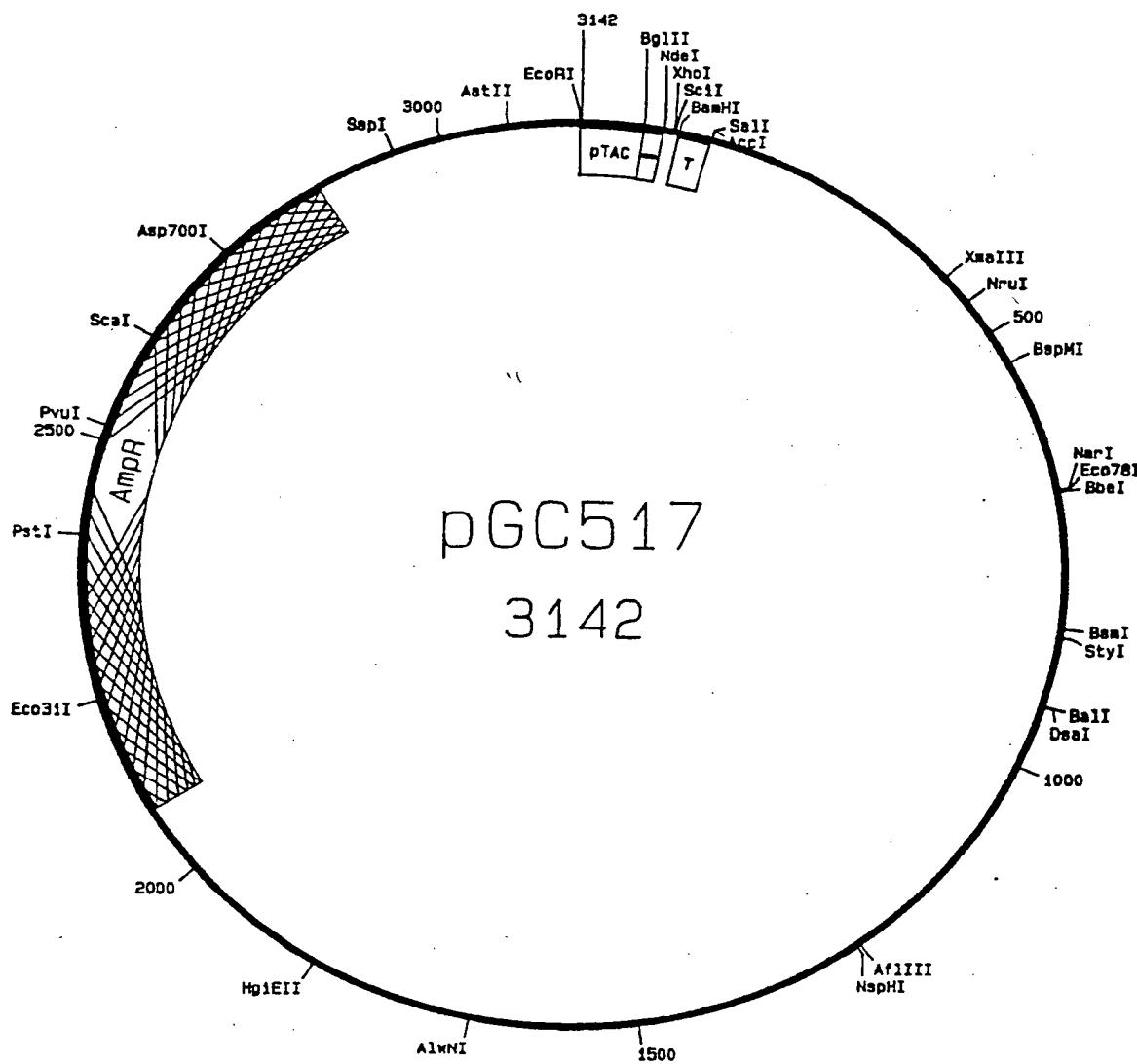
FIG. 3.



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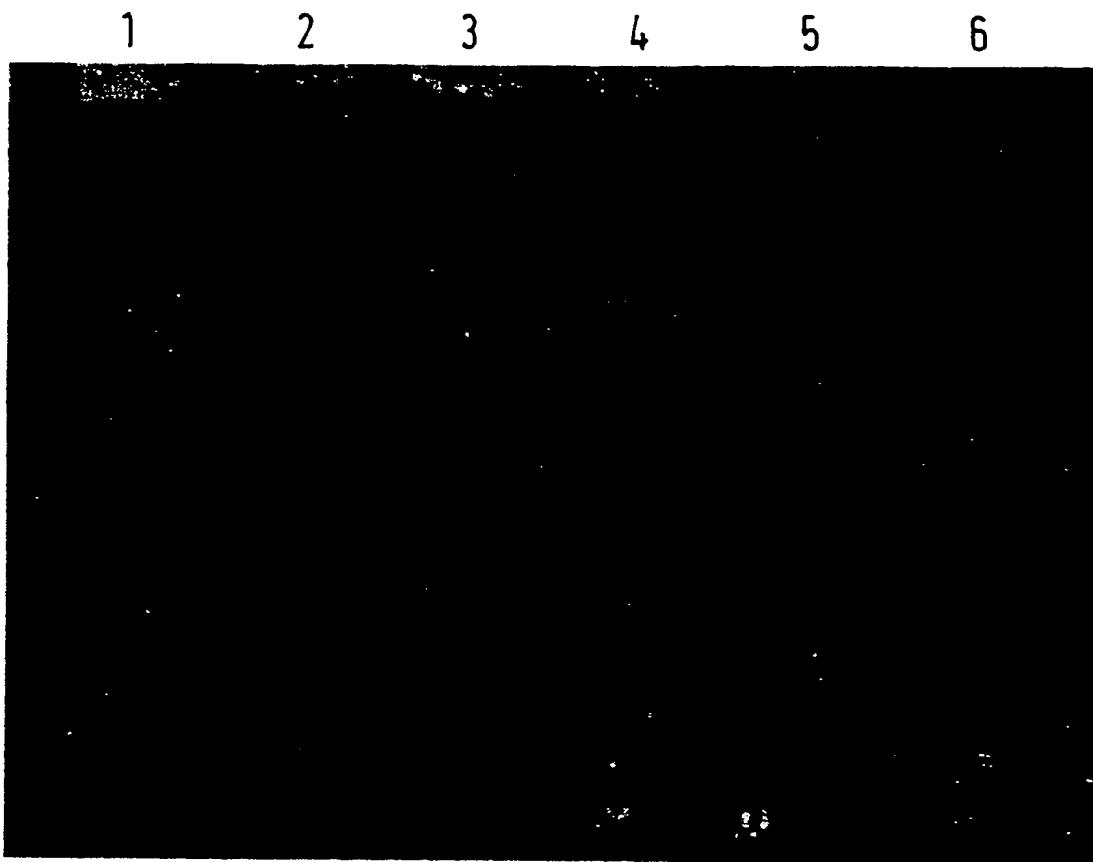
FIG. 4.



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FIG. 5.



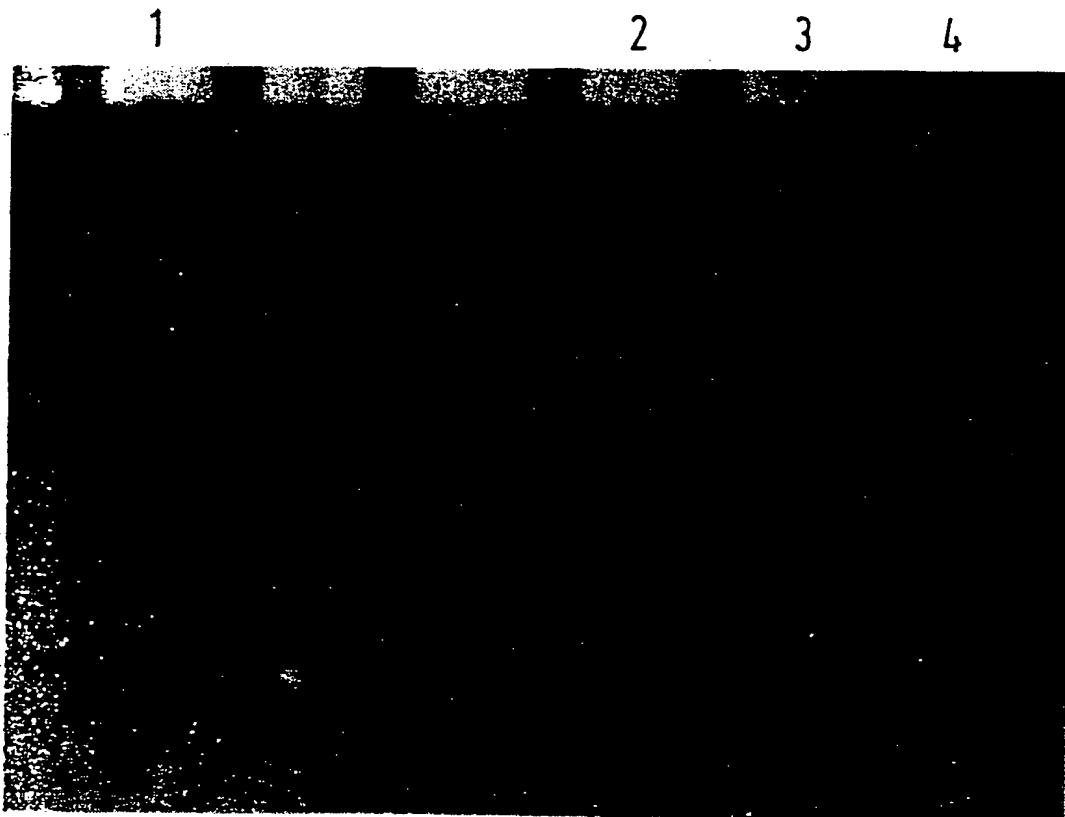
Zymograph of E. coli strains expressing streptokinase activity.

Lane 1. E. coli JM103 pKJ2 uninduced. Lane 2. E. coli JM103 pKJ2 IPTG induced. Lane 3. E. coli HW1110 pLGC1 uninduced. Lane 4. E. coli HW1110 pLGC1 IPTG induced. Lane 5. E. coli HW1110 pLGC2 uninduced. Lane 6. E. coli HW1110 pLGC2 IPTG induced.

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FIG. 6.



Zymograph of in vitro cleavage of the thrombin cleavable Streptokinase-streptokinase molecule by thrombin.

Lane 1. Streptokinase. Lane 2. 15-40% cut containing high molecular weight streptokinase activity, no thrombin. Lane 3, as 2 but 0.5 U/ml thrombin. Lane 4, as 2 but 5 U/ml thrombin.

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INTERNATIONAL SEARCH REPORT

International Application No. PCT/GB 90/01911

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) *

According to International Patent Classification (IPC) or to both National Classification and IPC
 IPC: 5 15/58, 15/62, 9/70, C 07 K 7/10, C 12 N 5/10, C 12 N 15/15,
 1/19, 1/21, A 61 K 37/64, 37/54

II. FIELDS SEARCHED

Minimum Documentation Searched ?

Classification System	Classification Symbols
IPC ⁵	C 12 N, C 07 K, A 61 K

Documentation Searched other than Minimum Documentation
 to the Extent that such Documents are Included in the Fields Searched *

III. DOCUMENTS CONSIDERED TO BE RELEVANT*

Category *	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X	EP, A, 0296413 (HOECHST) 28 December 1988 see example 6	1,7,8,12, 16-20,25, 27,28
Y	---	15
Y	EP, A, 0323149 (ELI LILLY) 5 July 1989 see page 13, lines 19-30; page 16, lines 5-13 ---	15
X	EP, A, 0292009 (ZYMOGENETICS) 23 November 1988 see page 3, lines 1-31; page 3, lines 57-58; page 6, line 48 - page 7, line 8; page 8, line 45 - page 9, line 15; page 22, section D; page 7, line 54 - page 8, line 2, examples 8,10,11; page 26, lines 38-45	1,7,8,12, 16-25,27,28
Y	---	2 ./.

* Special categories of cited documents: ¹⁰

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the International filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the International filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search

10th March 1991

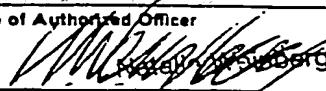
Date of Mailing of this International Search Report

08.05.91

International Searching Authority

EUROPEAN PATENT OFFICE

Signature of Authorized Officer



III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category *	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages	Relevant to Claim No.
A	EP, A, 0227938 (HOECHST) 8 July 1987 see page 3, lines 25-32; examples 1,2,4	3,9-12,25, 27,28
A	Mol Gen Genet, volume 212, 1988. MGG Springer-Verlag, C. Klessen et al.: "Tripartite streptokinase gene fusion vectors for gram-positive and gram-negative procaryotes", pages 295-300 see the whole document	4
A	EP, A, 0330700 (SAGAMI) 6 September 1989 see page 3, line 52 - page 4, line 45; page 5, line 20 - page 6, line 57	1,12

FURTHER INFORMATION CONTINUED FR M THE SECOND SHEET**V. OBSERVATIONS WHERE CERTAIN CLAIMS WERE FOUND UNSEARCHABLE¹**

This International search report has not been established in respect of certain claims under Article 17(2) (a) for the following reasons:

1. Claim numbers 26..... because they relate to subject matter not required to be searched by this Authority, namely:

see PCT Rule 39.1(iv)

2. Claim numbers....., because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claim numbers....., because they are dependent claims and are not drafted in accordance with the second and third sentences of PCT Rule 6.4(a).

VI. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING²

This International Searching Authority found multiple inventions in this International application as follows:

1. As all required additional search fees were timely paid by the applicant, this International search report covers all searchable claims of the International application.

2. As only some of the required additional search fees were timely paid by the applicant, this International search report covers only those claims of the International application for which fees were paid, specifically claims:

3. No required additional search fees were timely paid by the applicant. Consequently, this International search report is restricted to the invention first mentioned in the claims; it is covered by claim numbers:

4. As all searchable claims could be searched without effort justifying an additional fee, the International Searching Authority did not invite payment of any additional fee.

Remark on Protest

The additional search fees were accompanied by applicant's protest.
 No protest accompanied the payment of additional search fees.

**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO.**

GB 9001911
SA 42783

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EDP file on 23/04/91.
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

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